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(21) International Application Number: PCT/US97/18293 (22) International Filing Date: 7 October 1997 (07.10.97) (30) Priority Data: 08/730,510 11 October 1996 (11.10.96) US 08/818,112 13 March 1997 (13.03.97) US (71) Applicant: CORIXA CORPORATION [US/US]; 1124 Columbia Street, Seattle, WA 98104 (US). (72) Inventors: REED, Steven, G.; 2843 - 122nd Place N.E., Bellevue, WA 98005 (US). SKEIKY, Yasir, A., W.; 8327 - 25th Avenue N.W., Seattle, WA 98107 (US). DILLON, Davin, C.; 21607 N.E. 24th Street, Redmond, WA 98053 (US). CAMPOS-NETO, Antonio; 9308 Midship Court N.E., Bainbridge Island, WA 98021 (US). HOUGHTON, Raymond; 2636 - 242nd Place S.E., Bothell, WA 98021 (US). VEDVICK, Thomas, S.; 124 South 300th Place, Federal Way, WA 98003 (US). TWARDZIK, Daniel, R.; 10195 South Beach Drive, Bainbridge Island, WA 98110 (US). LODES, Michael, J.; 9223 - 36th Avenue S.W., Seattle, WA 98126 (US).	(74) Agents: MAKI, David, J. et al.; Seed and Berry LLP, 6300 Columbia Center, 701 Fifth Avenue, Seattle, WA 98104-7092 (US). (81) Designated States: AL, AM, AT, AU, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, UZ, VN, YU, ARIPO patent (GH, KE, LS, MW, SD, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG). Published <i>Without international search report and to be republished upon receipt of that report.</i>	
(54) Title: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY AND DIAGNOSIS OF TUBERCULOSIS (57) Abstract Compounds and methods for inducing protective immunity against tuberculosis are disclosed. The compounds provided include polypeptides that contain at least one immunogenic portion of one or more <i>M. tuberculosis</i> proteins and DNA molecules encoding such polypeptides. Such compounds may be formulated into vaccines and/or pharmaceutical compositions for immunization against <i>M. tuberculosis</i> infection, or may be used for the diagnosis of tuberculosis.		

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COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
AND DIAGNOSIS OF TUBERCULOSIS

5 TECHNICAL FIELD

The present invention relates generally to detecting, treating and preventing *Mycobacterium tuberculosis* infection. The invention is more particularly related to polypeptides comprising a *Mycobacterium tuberculosis* antigen, or a portion or other variant thereof, and the use of such polypeptides for diagnosing and vaccinating
10 against *Mycobacterium tuberculosis* infection.

BACKGROUND OF THE INVENTION

Tuberculosis is a chronic, infectious disease, that is generally caused by infection with *Mycobacterium tuberculosis*. It is a major disease in developing
15 countries, as well as an increasing problem in developed areas of the world, with about 8 million new cases and 3 million deaths each year. Although the infection may be asymptomatic for a considerable period of time, the disease is most commonly manifested as an acute inflammation of the lungs, resulting in fever and a nonproductive cough. If left untreated, serious complications and death typically result.

20 Although tuberculosis can generally be controlled using extended antibiotic therapy, such treatment is not sufficient to prevent the spread of the disease. Infected individuals may be asymptomatic, but contagious, for some time. In addition, although compliance with the treatment regimen is critical, patient behavior is difficult to monitor. Some patients do not complete the course of treatment, which can lead to
25 ineffective treatment and the development of drug resistance.

Inhibiting the spread of tuberculosis requires effective vaccination and accurate, early diagnosis of the disease. Currently, vaccination with live bacteria is the most efficient method for inducing protective immunity. The most common *Mycobacterium* employed for this purpose is *Bacillus Calmette-Guerin* (BCG), an
30 avirulent strain of *Mycobacterium bovis*. However, the safety and efficacy of BCG is a source of controversy and some countries, such as the United States, do not vaccinate

the general public. Diagnosis is commonly achieved using a skin test, which involves intradermal exposure to tuberculin PPD (protein-purified derivative). Antigen-specific T cell responses result in measurable induration at the injection site by 48-72 hours after injection, which indicates exposure to Mycobacterial antigens. Sensitivity and specificity have, however, been a problem with this test, and individuals vaccinated with BCG cannot be distinguished from infected individuals.

While macrophages have been shown to act as the principal effectors of *M. tuberculosis* immunity, T cells are the predominant inducers of such immunity. The essential role of T cells in protection against *M. tuberculosis* infection is illustrated by the frequent occurrence of *M. tuberculosis* in AIDS patients, due to the depletion of CD4 T cells associated with human immunodeficiency virus (HIV) infection. Mycobacterium-reactive CD4 T cells have been shown to be potent producers of gamma-interferon (IFN- γ), which, in turn, has been shown to trigger the anti-mycobacterial effects of macrophages in mice. While the role of IFN- γ in humans is less clear, studies have shown that 1,25-dihydroxy-vitamin D3, either alone or in combination with IFN- γ or tumor necrosis factor-alpha, activates human macrophages to inhibit *M. tuberculosis* infection. Furthermore, it is known that IFN- γ stimulates human macrophages to make 1,25-dihydroxy-vitamin D3. Similarly, IL-12 has been shown to play a role in stimulating resistance to *M. tuberculosis* infection. For a review of the immunology of *M. tuberculosis* infection see Chan and Kaufmann in *Tuberculosis: Pathogenesis, Protection and Control*, Bloom (ed.), ASM Press, Washington, DC, 1994.

Accordingly, there is a need in the art for improved vaccines and methods for preventing, treating and detecting tuberculosis. The present invention fulfills these needs and further provides other related advantages.

SUMMARY OF THE INVENTION

Briefly stated, this invention provides compounds and methods for preventing and diagnosing tuberculosis. In one aspect, polypeptides are provided comprising an immunogenic portion of a soluble *M. tuberculosis* antigen, or a variant of such an antigen that differs only in conservative substitutions and/or modifications. In

one embodiment of this aspect, the soluble antigen has one of the following N-terminal sequences:

- (a) Asp-Pro-Val-Asp-Ala-Val-Ile-Asn-Thr-Thr-Cys-Asn-Tyr-Gly-Gln-Val-Val-Ala-Ala-Leu; (SEQ ID No. 120)
- 5 (b) Ala-Val-Glu-Ser-Gly-Met-Leu-Ala-Leu-Gly-Thr-Pro-Ala-Pro-Ser; (SEQ ID No. 121)
- (c) Ala-Ala-Met-Lys-Pro-Arg-Thr-Gly-Asp-Gly-Pro-Leu-Glu-Ala-Ala-Lys-Glu-Gly-Arg; (SEQ ID No. 122)
- (d) Tyr-Tyr-Trp-Cys-Pro-Gly-Gln-Pro-Phe-Asp-Pro-Ala-Trp-Gly-Pro; (SEQ ID No. 123)
- 10 (e) Asp-Ile-Gly-Ser-Glu-Ser-Thr-Glu-Asp-Gln-Gln-Xaa-Ala-Val; (SEQ ID No. 124)
- (f) Ala-Glu-Glu-Ser-Ile-Ser-Thr-Xaa-Glu-Xaa-Ile-Val-Pro; (SEQ ID No. 125)
- 15 (g) Asp-Pro-Glu-Pro-Ala-Pro-Pro-Val-Pro-Thr-Thr-Ala-Ala-Ser-Pro-Pro-Ser; (SEQ ID No. 126)
- (h) Ala-Pro-Lys-Thr-Tyr-Xaa-Glu-Glu-Leu-Lys-Gly-Thr-Asp-Thr-Gly; (SEQ ID No. 127)
- (i) Asp-Pro-Ala-Ser-Ala-Pro-Asp-Val-Pro-Thr-Ala-Ala-Gln-Leu-Thr-Ser-Leu-Leu-Asn-Ser-Leu-Ala-Asp-Pro-Asn-Val-Ser-Phe-Ala-Asn; (SEQ ID No. 128)
- 20 (j) Xaa-Asp-Ser-Glu-Lys-Ser-Ala-Thr-Ile-Lys-Val-Thr-Asp-Ala-Ser; (SEQ ID No. 134)
- (k) Ala-Gly-Asp-Thr-Xaa-Ile-Tyr-Ile-Val-Gly-Asn-Leu-Thr-Ala-Asp; (SEQ ID No. 135) or
- 25 (l) Ala-Pro-Glu-Ser-Gly-Ala-Gly-Leu-Gly-Gly-Thr-Val-Gln-Ala-Gly; (SEQ ID No. 136)

wherein Xaa may be any amino acid.

In a related aspect, polypeptides are provided comprising an immunogenic portion of an *M. tuberculosis* antigen, or a variant of such an antigen that

differs only in conservative substitutions and/or modifications, the antigen having one of the following N-terminal sequences:

- (m) Xaa-Tyr-Ile-Ala-Tyr-Xaa-Thr-Thr-Ala-Gly-Ile-Val-Pro-Gly-Lys-Ile-Asn-Val-His-Leu-Val; (SEQ ID No. 137) or
- 5 (n) Asp-Pro-Pro-Asp-Pro-His-Gln-Xaa-Asp-Met-Thr-Lys-Gly-Tyr-Tyr-Pro-Gly-Gly-Arg-Arg-Xaa-Phe; (SEQ ID No. 129)

wherein Xaa may be any amino acid.

In another embodiment, the soluble *M. tuberculosis* antigen comprises an amino acid sequence encoded by a DNA sequence selected from the group consisting of the sequences recited in SEQ ID Nos.: 1, 2, 4-10, 13-25, 52, 99 and 101, the complements of said sequences, and DNA sequences that hybridize to a sequence recited in SEQ ID Nos.: 1, 2, 4-10, 13-25, 52, 99 and 101 or a complement thereof under moderately stringent conditions.

In a related aspect, the polypeptides comprise an immunogenic portion of a *M. tuberculosis* antigen, or a variant of such an antigen that differs only in conservative substitutions and/or modifications, wherein the antigen comprises an amino acid sequence encoded by a DNA sequence selected from the group consisting of the sequences recited in SEQ ID Nos.: 26-51, 138, 139, 163-183 and 201, the complements of said sequences, and DNA sequences that hybridize to a sequence recited in SEQ ID Nos.: 26-51, 138, 139, 163-183 and 201 or a complement thereof under moderately stringent conditions.

In related aspects, DNA sequences encoding the above polypeptides, expression vectors comprising these DNA sequences and host cells transformed or transfected with such expression vectors are also provided.

25 In another aspect, the present invention provides fusion proteins comprising a first and a second inventive polypeptide or, alternatively, an inventive polypeptide and a known *M. tuberculosis* antigen.

Within other aspects, the present invention provides pharmaceutical compositions that comprise one or more of the above polypeptides, or a DNA molecule encoding such polypeptides, and a physiologically acceptable carrier. The invention

30

also provides vaccines comprising one or more of the polypeptides as described above and a non-specific immune response enhancer, together with vaccines comprising one or more DNA sequences encoding such polypeptides and a non-specific immune response enhancer.

5 In yet another aspect, methods are provided for inducing protective immunity in a patient, comprising administering to a patient an effective amount of one or more of the above polypeptides.

In further aspects of this invention, methods and diagnostic kits are provided for detecting tuberculosis in a patient. The methods comprise contacting
10 dermal cells of a patient with one or more of the above polypeptides and detecting an immune response on the patient's skin. The diagnostic kits comprise one or more of the above polypeptides in combination with an apparatus sufficient to contact the polypeptide with the dermal cells of a patient.

In yet other aspects, methods are provided for detecting tuberculosis in a
15 patient, such methods comprising contacting dermal cells of a patient with one or more polypeptides encoded by a DNA sequence selected from the group consisting of SEQ ID Nos.: 3, 11, 12, 140, 141, 156-160, 189-193, 199, 200 and 203, the complements of said sequences, and DNA sequences that hybridize to a sequence recited in SEQ ID Nos.: 3, 11, 12, 140, 141, 156-160, 189-193, 199, 200 and 203; and detecting an
20 immune response on the patient's skin. Diagnostic kits for use in such methods are also provided.

These and other aspects of the present invention will become apparent upon reference to the following detailed description and attached drawings. All
25 references disclosed herein are hereby incorporated by reference in their entirety as if each was incorporated individually.

BRIEF DESCRIPTION OF THE DRAWINGS AND SEQUENCE IDENTIFIERS

Figure 1A and B illustrate the stimulation of proliferation and interferon-
30 γ production in T cells derived from a first and a second *M. tuberculosis*-immune donor, respectively, by the 14 Kd, 20 Kd and 26 Kd antigens described in Example 1.

Figure 2 illustrates the stimulation of proliferation and interferon- γ production in T cells derived from an *M. tuberculosis*-immune individual by the two representative polypeptides TbRa3 and TbRa9.

Figures 3A-D illustrate the reactivity of antisera raised against secretory
5 *M. tuberculosis* proteins, the known *M. tuberculosis* antigen 85b and the inventive antigens Tb38-1 and TbH-9, respectively, with *M. tuberculosis* lysate (lane 2), *M. tuberculosis* secretory proteins (lane 3), recombinant Tb38-1 (lane 4), recombinant TbH-9 (lane 5) and recombinant 85b (lane 5).

Figure 4A illustrates the stimulation of proliferation in a TbH-9-specific
10 T cell clone by secretory *M. tuberculosis* proteins, recombinant TbH-9 and a control antigen, TbRa11.

Figure 4B illustrates the stimulation of interferon- γ production in a TbH-9-specific T cell clone by secretory *M. tuberculosis* proteins, PPD and recombinant TbH-9.

15 Figures 5A and B illustrate the stimulation of proliferation and interferon- γ production in TbH9-specific T cells by the fusion protein TbH9-Tb38-1.

Figures 6A and B illustrate the stimulation of proliferation and interferon- γ production in Tb38-1-specific T cells by the fusion protein TbH9-Tb38-1.

Figures 7A and B illustrate the stimulation of proliferation and
20 interferon- γ production in T cells previously shown to respond to both TbH-9 and Tb38-1 by the fusion protein TbH9-Tb38-1.

Figures 8A and B illustrate the stimulation of proliferation and interferon- γ production in T cells derived from a first *M. tuberculosis*-immune individual by the representative polypeptides XP-1, RDIF6, RDIF8, RDIF10 and
25 RDIF11.

Figures 9A and B illustrate the stimulation of proliferation and interferon- γ production in T cells derived from a second *M. tuberculosis*-immune individual by the representative polypeptides XP-1, RDIF6, RDIF8, RDIF10 and RDIF11.

- SEQ. ID NO. 1 is the DNA sequence of TbRa1.
SEQ. ID NO. 2 is the DNA sequence of TbRa10.
SEQ. ID NO. 3 is the DNA sequence of TbRa11.
SEQ. ID NO. 4 is the DNA sequence of TbRa12.
5 SEQ. ID NO. 5 is the DNA sequence of TbRa13.
SEQ. ID NO. 6 is the DNA sequence of TbRa16.
SEQ. ID NO. 7 is the DNA sequence of TbRa17.
SEQ. ID NO. 8 is the DNA sequence of TbRa18.
SEQ. ID NO. 9 is the DNA sequence of TbRa19.
10 SEQ. ID NO. 10 is the DNA sequence of TbRa24.
SEQ. ID NO. 11 is the DNA sequence of TbRa26.
SEQ. ID NO. 12 is the DNA sequence of TbRa28.
SEQ. ID NO. 13 is the DNA sequence of TbRa29.
SEQ. ID NO. 14 is the DNA sequence of TbRa2A.
15 SEQ. ID NO. 15 is the DNA sequence of TbRa3.
SEQ. ID NO. 16 is the DNA sequence of TbRa32.
SEQ. ID NO. 17 is the DNA sequence of TbRa35.
SEQ. ID NO. 18 is the DNA sequence of TbRa36.
SEQ. ID NO. 19 is the DNA sequence of TbRa4.
20 SEQ. ID NO. 20 is the DNA sequence of TbRa9.
SEQ. ID NO. 21 is the DNA sequence of TbRaB.
SEQ. ID NO. 22 is the DNA sequence of TbRaC.
SEQ. ID NO. 23 is the DNA sequence of TbRaD.
SEQ. ID NO. 24 is the DNA sequence of YYWCPG.
25 SEQ. ID NO. 25 is the DNA sequence of AAMK.
SEQ. ID NO. 26 is the DNA sequence of TbL-23.
SEQ. ID NO. 27 is the DNA sequence of TbL-24.
SEQ. ID NO. 28 is the DNA sequence of TbL-25.
SEQ. ID NO. 29 is the DNA sequence of TbL-28.
30 SEQ. ID NO. 30 is the DNA sequence of TbL-29.

- SEQ. ID NO. 31 is the DNA sequence of TbH-5.
- SEQ. ID NO. 32 is the DNA sequence of TbH-8.
- SEQ. ID NO. 33 is the DNA sequence of TbH-9.
- SEQ. ID NO. 34 is the DNA sequence of TbM-1.
- 5 SEQ. ID NO. 35 is the DNA sequence of TbM-3.
- SEQ. ID NO. 36 is the DNA sequence of TbM-6.
- SEQ. ID NO. 37 is the DNA sequence of TbM-7.
- SEQ. ID NO. 38 is the DNA sequence of TbM-9.
- SEQ. ID NO. 39 is the DNA sequence of TbM-12.
- 10 SEQ. ID NO. 40 is the DNA sequence of TbM-13.
- SEQ. ID NO. 41 is the DNA sequence of TbM-14.
- SEQ. ID NO. 42 is the DNA sequence of TbM-15.
- SEQ. ID NO. 43 is the DNA sequence of TbH-4.
- SEQ. ID NO. 44 is the DNA sequence of TbH-4-FWD.
- 15 SEQ. ID NO. 45 is the DNA sequence of TbH-12.
- SEQ. ID NO. 46 is the DNA sequence of Tb38-1.
- SEQ. ID NO. 47 is the DNA sequence of Tb38-4.
- SEQ. ID NO. 48 is the DNA sequence of TbL-17.
- SEQ. ID NO. 49 is the DNA sequence of TbL-20.
- 20 SEQ. ID NO. 50 is the DNA sequence of TbL-21.
- SEQ. ID NO. 51 is the DNA sequence of TbH-16.
- SEQ. ID NO. 52 is the DNA sequence of DPEP.
- SEQ. ID NO. 53 is the deduced amino acid sequence of DPEP.
- SEQ. ID NO. 54 is the protein sequence of DPV N-terminal Antigen.
- 25 SEQ. ID NO. 55 is the protein sequence of AVGS N-terminal Antigen.
- SEQ. ID NO. 56 is the protein sequence of AAMK N-terminal Antigen.
- SEQ. ID NO. 57 is the protein sequence of YYWC N-terminal Antigen.
- SEQ. ID NO. 58 is the protein sequence of DIGS N-terminal Antigen.
- SEQ. ID NO. 59 is the protein sequence of AEES N-terminal Antigen.
- 30 SEQ. ID NO. 60 is the protein sequence of DPEP N-terminal Antigen.

- SEQ. ID NO. 61 is the protein sequence of APKT N-terminal Antigen.
SEQ. ID NO. 62 is the protein sequence of DPAS N-terminal Antigen.
SEQ. ID NO. 63 is the deduced amino acid sequence of TbRa1.
SEQ. ID NO. 64 is the deduced amino acid sequence of TbRa10.
5 SEQ. ID NO. 65 is the deduced amino acid sequence of TbRa11.
SEQ. ID NO. 66 is the deduced amino acid sequence of TbRa12.
SEQ. ID NO. 67 is the deduced amino acid sequence of TbRa13.
SEQ. ID NO. 68 is the deduced amino acid sequence of TbRa16.
SEQ. ID NO. 69 is the deduced amino acid sequence of TbRa17.
10 SEQ. ID NO. 70 is the deduced amino acid sequence of TbRa18.
SEQ. ID NO. 71 is the deduced amino acid sequence of TbRa19.
SEQ. ID NO. 72 is the deduced amino acid sequence of TbRa24.
SEQ. ID NO. 73 is the deduced amino acid sequence of TbRa26.
SEQ. ID NO. 74 is the deduced amino acid sequence of TbRa28.
15 SEQ. ID NO. 75 is the deduced amino acid sequence of TbRa29.
SEQ. ID NO. 76 is the deduced amino acid sequence of TbRa2A.
SEQ. ID NO. 77 is the deduced amino acid sequence of TbRa3.
SEQ. ID NO. 78 is the deduced amino acid sequence of TbRa32.
SEQ. ID NO. 79 is the deduced amino acid sequence of TbRa35.
20 SEQ. ID NO. 80 is the deduced amino acid sequence of TbRa36.
SEQ. ID NO. 81 is the deduced amino acid sequence of TbRa4.
SEQ. ID NO. 82 is the deduced amino acid sequence of TbRa9.
SEQ. ID NO. 83 is the deduced amino acid sequence of TbRaB.
SEQ. ID NO. 84 is the deduced amino acid sequence of TbRaC.
25 SEQ. ID NO. 85 is the deduced amino acid sequence of TbRaD.
SEQ. ID NO. 86 is the deduced amino acid sequence of YYWCPG.
SEQ. ID NO. 87 is the deduced amino acid sequence of TbAAMK.
SEQ. ID NO. 88 is the deduced amino acid sequence of Tb38-1.
SEQ. ID NO. 89 is the deduced amino acid sequence of TbH-4.
30 SEQ. ID NO. 90 is the deduced amino acid sequence of TbH-8.

- SEQ. ID NO. 91 is the deduced amino acid sequence of TbH-9.
- SEQ. ID NO. 92 is the deduced amino acid sequence of TbH-12.
- SEQ. ID NO. 93 is the amino acid sequence of Tb38-1 Peptide 1.
- SEQ. ID NO. 94 is the amino acid sequence of Tb38-1 Peptide 2.
- 5 SEQ. ID NO. 95 is the amino acid sequence of Tb38-1 Peptide 3.
- SEQ. ID NO. 96 is the amino acid sequence of Tb38-1 Peptide 4.
- SEQ. ID NO. 97 is the amino acid sequence of Tb38-1 Peptide 5.
- SEQ. ID NO. 98 is the amino acid sequence of Tb38-1 Peptide 6.
- SEQ. ID NO. 99 is the DNA sequence of DPAS.
- 10 SEQ. ID NO. 100 is the deduced amino acid sequence of DPAS.
- SEQ. ID NO. 101 is the DNA sequence of DPV.
- SEQ. ID NO. 102 is the deduced amino acid sequence of DPV.
- SEQ. ID NO. 103 is the DNA sequence of ESAT-6.
- SEQ. ID NO. 104 is the deduced amino acid sequence of ESAT-6.
- 15 SEQ. ID NO. 105 is the DNA sequence of TbH-8-2.
- SEQ. ID NO. 106 is the DNA sequence of TbH-9FL.
- SEQ. ID NO. 107 is the deduced amino acid sequence of TbH-9FL.
- SEQ. ID NO. 108 is the DNA sequence of TbH-9-1.
- SEQ. ID NO. 109 is the deduced amino acid sequence of TbH-9-1.
- 20 SEQ. ID NO. 110 is the DNA sequence of TbH-9-4.
- SEQ. ID NO. 111 is the deduced amino acid sequence of TbH-9-4.
- SEQ. ID NO. 112 is the DNA sequence of Tb38-1F2 IN.
- SEQ. ID NO. 113 is the DNA sequence of Tb38-2F2 RP.
- SEQ. ID NO. 114 is the deduced amino acid sequence of Tb37-FL.
- 25 SEQ. ID NO. 115 is the deduced amino acid sequence of Tb38-IN.
- SEQ. ID NO. 116 is the DNA sequence of Tb38-1F3.
- SEQ. ID NO. 117 is the deduced amino acid sequence of Tb38-1F3.
- SEQ. ID NO. 118 is the DNA sequence of Tb38-1F5.
- SEQ. ID NO. 119 is the DNA sequence of Tb38-1F6.
- 30 SEQ. ID NO. 120 is the deduced N-terminal amino acid sequence of DPV.

- SEQ. ID NO. 121 is the deduced N-terminal amino acid sequence of AVGS.
SEQ. ID NO. 122 is the deduced N-terminal amino acid sequence of AAMK.
SEQ. ID NO. 123 is the deduced N-terminal amino acid sequence of YYWC.
SEQ. ID NO. 124 is the deduced N-terminal amino acid sequence of DIGS.
5 SEQ. ID NO. 125 is the deduced N-terminal amino acid sequence of AEES.
SEQ. ID NO. 126 is the deduced N-terminal amino acid sequence of DPEP.
SEQ. ID NO. 127 is the deduced N-terminal amino acid sequence of APKT.
SEQ. ID NO. 128 is the deduced amino acid sequence of DPAS.
SEQ. ID NO. 129 is the protein sequence of DPPD N-terminal Antigen.
10 SEQ ID NO. 130-133 are the protein sequences of four DPPD cyanogen
bromide fragments.
SEQ ID NO. 134 is the N-terminal protein sequence of XDS antigen.
SEQ ID NO. 135 is the N-terminal protein sequence of AGD antigen.
SEQ ID NO. 136 is the N-terminal protein sequence of APE antigen.
15 SEQ ID NO. 137 is the N-terminal protein sequence of XYI antigen.
SEQ ID NO. 138 is the DNA sequence of TbH-29.
SEQ ID NO. 139 is the DNA sequence of TbH-30.
SEQ ID NO. 140 is the DNA sequence of TbH-32.
SEQ ID NO. 141 is the DNA sequence of TbH-33.
20 SEQ ID NO. 142 is the predicted amino acid sequence of TbH-29.
SEQ ID NO. 143 is the predicted amino acid sequence of TbH-30.
SEQ ID NO. 144 is the predicted amino acid sequence of TbH-32.
SEQ ID NO. 145 is the predicted amino acid sequence of TbH-33.
SEQ ID NO: 146-151 are PCR primers used in the preparation of a fusion
25 protein containing TbRa3, 38 kD and Tb38-1.
SEQ ID NO: 152 is the DNA sequence of the fusion protein containing TbRa3,
38 kD and Tb38-1.
SEQ ID NO: 153 is the amino acid sequence of the fusion protein containing
TbRa3, 38 kD and Tb38-1.
30 SEQ ID NO: 154 is the DNA sequence of the *M. tuberculosis* antigen 38 kD.

SEQ ID NO: 155 is the amino acid sequence of the *M. tuberculosis* antigen 38 kD.

SEQ ID NO: 156 is the DNA sequence of XP14.

SEQ ID NO: 157 is the DNA sequence of XP24.

5 SEQ ID NO: 158 is the DNA sequence of XP31.

SEQ ID NO: 159 is the 5' DNA sequence of XP32.

SEQ ID NO: 160 is the 3' DNA sequence of XP32.

SEQ ID NO: 161 is the predicted amino acid sequence of XP14.

10 SEQ ID NO: 162 is the predicted amino acid sequence encoded by the reverse complement of XP14.

SEQ ID NO: 163 is the DNA sequence of XP27.

SEQ ID NO: 164 is the DNA sequence of XP36.

SEQ ID NO: 165 is the 5' DNA sequence of XP4.

SEQ ID NO: 166 is the 5' DNA sequence of XP5.

15 SEQ ID NO: 167 is the 5' DNA sequence of XP17.

SEQ ID NO: 168 is the 5' DNA sequence of XP30.

SEQ ID NO: 169 is the 5' DNA sequence of XP2.

SEQ ID NO: 170 is the 3' DNA sequence of XP2.

SEQ ID NO: 171 is the 5' DNA sequence of XP3.

20 SEQ ID NO: 172 is the 3' DNA sequence of XP3.

SEQ ID NO: 173 is the 5' DNA sequence of XP6.

SEQ ID NO: 174 is the 3' DNA sequence of XP6.

SEQ ID NO: 175 is the 5' DNA sequence of XP18.

SEQ ID NO: 176 is the 3' DNA sequence of XP18.

25 SEQ ID NO: 177 is the 5' DNA sequence of XP19.

SEQ ID NO: 178 is the 3' DNA sequence of XP19.

SEQ ID NO: 179 is the 5' DNA sequence of XP22.

SEQ ID NO: 180 is the 3' DNA sequence of XP22.

SEQ ID NO: 181 is the 5' DNA sequence of XP25.

30 SEQ ID NO: 182 is the 3' DNA sequence of XP25.

SEQ ID NO: 183 is the full-length DNA sequence of TbH4-XP1.

SEQ ID NO: 184 is the predicted amino acid sequence of TbH4-XP1.

SEQ ID NO: 185 is the predicted amino acid sequence encoded by the reverse complement of TbH4-XP1.

5 SEQ ID NO: 186 is a first predicted amino acid sequence encoded by XP36.

SEQ ID NO: 187 is a second predicted amino acid sequence encoded by XP36.

SEQ ID NO: 188 is the predicted amino acid sequence encoded by the reverse complement of XP36.

SEQ ID NO: 189 is the DNA sequence of RDIF2.

10 SEQ ID NO: 190 is the DNA sequence of RDIF5.

SEQ ID NO: 191 is the DNA sequence of RDIF8.

SEQ ID NO: 192 is the DNA sequence of RDIF10.

SEQ ID NO: 193 is the DNA sequence of RDIF11.

SEQ ID NO: 194 is the predicted amino acid sequence of RDIF2.

15 SEQ ID NO: 195 is the predicted amino acid sequence of RDIF5.

SEQ ID NO: 196 is the predicted amino acid sequence of RDIF8.

SEQ ID NO: 197 is the predicted amino acid sequence of RDIF10.

SEQ ID NO: 198 is the predicted amino acid sequence of RDIF11.

SEQ ID NO: 199 is the 5' DNA sequence of RDIF12.

20 SEQ ID NO: 200 is the 3' DNA sequence of RDIF12.

SEQ ID NO: 201 is the DNA sequence of RDIF7.

SEQ ID NO: 202 is the predicted amino acid sequence of RDIF7.

SEQ ID NO: 203 is the DNA sequence of DIF2-1.

SEQ ID NO: 204 is the predicted amino acid sequence of DIF2-1.

25 SEQ ID NO: 205-212 are PCR primers used in the preparation of a fusion protein containing TbRa3, 38 kD, Tb38-1 and DPEP (hereinafter referred to as TbF-2).

SEQ ID NO: 213 is the DNA sequence of the fusion protein TbF-2.

SEQ ID NO: 214 is the amino acid sequence of the fusion protein TbF-2.

DETAILED DESCRIPTION OF THE INVENTION

As noted above, the present invention is generally directed to compositions and methods for preventing, treating and diagnosing tuberculosis. The compositions of the subject invention include polypeptides that comprise at least one immunogenic portion of a *M. tuberculosis* antigen, or a variant of such an antigen that differs only in conservative substitutions and/or modifications. Polypeptides within the scope of the present invention include, but are not limited to, immunogenic soluble *M. tuberculosis* antigens. A "soluble *M. tuberculosis* antigen" is a protein of *M. tuberculosis* origin that is present in *M. tuberculosis* culture filtrate. As used herein, the term "polypeptide" encompasses amino acid chains of any length, including full length proteins (*i.e.*, antigens), wherein the amino acid residues are linked by covalent peptide bonds. Thus, a polypeptide comprising an immunogenic portion of one of the above antigens may consist entirely of the immunogenic portion, or may contain additional sequences. The additional sequences may be derived from the native *M. tuberculosis* antigen or may be heterologous, and such sequences may (but need not) be immunogenic.

"Immunogenic," as used herein, refers to the ability to elicit an immune response (*e.g.*, cellular) in a patient, such as a human, and/or in a biological sample. In particular, antigens that are immunogenic (and immunogenic portions or other variants of such antigens) are capable of stimulating cell proliferation, interleukin-12 production and/or interferon- γ production in biological samples comprising one or more cells selected from the group of T cells, NK cells, B cells and macrophages, where the cells are derived from an *M. tuberculosis*-immune individual. Polypeptides comprising at least an immunogenic portion of one or more *M. tuberculosis* antigens may generally be used to detect tuberculosis or to induce protective immunity against tuberculosis in a patient.

The compositions and methods of this invention also encompass variants of the above polypeptides. A "variant," as used herein, is a polypeptide that differs from the native antigen only in conservative substitutions and/or modifications, such that the ability of the polypeptide to induce an immune response is retained. Such variants may generally be identified by modifying one of the above polypeptide

sequences, and evaluating the immunogenic properties of the modified polypeptide using, for example, the representative procedures described herein.

A "conservative substitution" is one in which an amino acid is substituted for another amino acid that has similar properties, such that one skilled in the art of peptide chemistry would expect the secondary structure and hydrophobic nature of the polypeptide to be substantially unchanged. In general, the following groups of amino acids represent conservative changes: (1) ala, pro, gly, glu, asp, gln, asn, ser, thr; (2) cys, ser, tyr, thr; (3) val, ile, leu, met, ala, phe; (4) lys, arg, his; and (5) phe, tyr, trp, his.

Variants may also (or alternatively) be modified by, for example, the deletion or addition of amino acids that have minimal influence on the immunogenic properties, secondary structure and hydrophobic nature of the polypeptide. For example, a polypeptide may be conjugated to a signal (or leader) sequence at the N-terminal end of the protein which co-translationally or post-translationally directs transfer of the protein. The polypeptide may also be conjugated to a linker or other sequence for ease of synthesis, purification or identification of the polypeptide (*e.g.*, poly-His), or to enhance binding of the polypeptide to a solid support. For example, a polypeptide may be conjugated to an immunoglobulin Fc region.

In a related aspect, combination polypeptides are disclosed. A "combination polypeptide" is a polypeptide comprising at least one of the above immunogenic portions and one or more additional immunogenic *M. tuberculosis* sequences, which are joined via a peptide linkage into a single amino acid chain. The sequences may be joined directly (*i.e.*, with no intervening amino acids) or may be joined by way of a linker sequence (*e.g.*, Gly-Cys-Gly) that does not significantly diminish the immunogenic properties of the component polypeptides.

In general, *M. tuberculosis* antigens, and DNA sequences encoding such antigens, may be prepared using any of a variety of procedures. For example, soluble antigens may be isolated from *M. tuberculosis* culture filtrate by procedures known to those of ordinary skill in the art, including anion-exchange and reverse phase chromatography. Purified antigens are then evaluated for their ability to elicit an

appropriate immune response (e.g., cellular) using, for example, the representative methods described herein. Immunogenic antigens may then be partially sequenced using techniques such as traditional Edman chemistry. See Edman and Berg, *Eur. J. Biochem.* 80:116-132, 1967.

5 Immunogenic antigens may also be produced recombinantly using a DNA sequence that encodes the antigen, which has been inserted into an expression vector and expressed in an appropriate host. DNA molecules encoding soluble antigens may be isolated by screening an appropriate *M. tuberculosis* expression library with anti-sera (e.g., rabbit) raised specifically against soluble *M. tuberculosis* antigens. DNA
10 sequences encoding antigens that may or may not be soluble may be identified by screening an appropriate *M. tuberculosis* genomic or cDNA expression library with sera obtained from patients infected with *M. tuberculosis*. Such screens may generally be performed using techniques well known to those of ordinary skill in the art, such as those described in Sambrook et al., *Molecular Cloning: A Laboratory Manual*, Cold
15 Spring Harbor Laboratories, Cold Spring Harbor, NY, 1989.

DNA sequences encoding soluble antigens may also be obtained by screening an appropriate *M. tuberculosis* cDNA or genomic DNA library for DNA sequences that hybridize to degenerate oligonucleotides derived from partial amino acid sequences of isolated soluble antigens. Degenerate oligonucleotide sequences for use in
20 such a screen may be designed and synthesized, and the screen may be performed, as described (for example) in Sambrook et al., *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratories, Cold Spring Harbor, NY, 1989 (and references cited therein). Polymerase chain reaction (PCR) may also be employed, using the above oligonucleotides in methods well known in the art, to isolate a nucleic acid probe from a
25 cDNA or genomic library. The library screen may then be performed using the isolated probe.

Alternatively, genomic or cDNA libraries derived from *M. tuberculosis* may be screened directly using peripheral blood mononuclear cells (PBMCs) or T cell lines or clones derived from one or more *M. tuberculosis*-immune individuals. In
30 general, PBMCs and/or T cells for use in such screens may be prepared as described

below. Direct library screens may generally be performed by assaying pools of expressed recombinant proteins for the ability to induce proliferation and/or interferon- γ production in T cells derived from an *M. tuberculosis*-immune individual. Alternatively, potential T cell antigens may be first selected based on antibody
5 reactivity, as described above.

Regardless of the method of preparation, the antigens (and immunogenic portions thereof) described herein (which may or may not be soluble) have the ability to induce an immunogenic response. More specifically, the antigens have the ability to induce proliferation and/or cytokine production (*i.e.*, interferon- γ and/or interleukin-12
10 production) in T cells, NK cells, B cells and/or macrophages derived from an *M. tuberculosis*-immune individual. The selection of cell type for use in evaluating an immunogenic response to a antigen will, of course, depend on the desired response. For example, interleukin-12 production is most readily evaluated using preparations containing B cells and/or macrophages. An *M. tuberculosis*-immune individual is one
15 who is considered to be resistant to the development of tuberculosis by virtue of having mounted an effective T cell response to *M. tuberculosis* (*i.e.*, substantially free of disease symptoms). Such individuals may be identified based on a strongly positive (*i.e.*, greater than about 10 mm diameter induration) intradermal skin test response to tuberculosis proteins (PPD) and an absence of any signs or symptoms of tuberculosis
20 disease. T cells, NK cells, B cells and macrophages derived from *M. tuberculosis*-immune individuals may be prepared using methods known to those of ordinary skill in the art. For example, a preparation of PBMCs (*i.e.*, peripheral blood mononuclear cells) may be employed without further separation of component cells. PBMCs may generally be prepared, for example, using density centrifugation through Ficoll™
25 (Winthrop Laboratories, NY). T cells for use in the assays described herein may also be purified directly from PBMCs. Alternatively, an enriched T cell line reactive against mycobacterial proteins, or T cell clones reactive to individual mycobacterial proteins, may be employed. Such T cell clones may be generated by, for example, culturing PBMCs from *M. tuberculosis*-immune individuals with mycobacterial proteins for a
30 period of 2-4 weeks. This allows expansion of only the mycobacterial protein-specific

T cells, resulting in a line composed solely of such cells. These cells may then be cloned and tested with individual proteins, using methods known to those of ordinary skill in the art, to more accurately define individual T cell specificity. In general, antigens that test positive in assays for proliferation and/or cytokine production (*i.e.*,
5 interferon- γ and/or interleukin-12 production) performed using T cells, NK cells, B cells and/or macrophages derived from an *M. tuberculosis*-immune individual are considered immunogenic. Such assays may be performed, for example, using the representative procedures described below. Immunogenic portions of such antigens may be identified using similar assays, and may be present within the polypeptides described herein.

10 The ability of a polypeptide (*e.g.*, an immunogenic antigen, or a portion or other variant thereof) to induce cell proliferation is evaluated by contacting the cells (*e.g.*, T cells and/or NK cells) with the polypeptide and measuring the proliferation of the cells. In general, the amount of polypeptide that is sufficient for evaluation of about 10^5 cells ranges from about 10 ng/mL to about 100 μ g/mL and preferably is about
15 10 μ g/mL. The incubation of polypeptide with cells is typically performed at 37°C for about six days. Following incubation with polypeptide, the cells are assayed for a proliferative response, which may be evaluated by methods known to those of ordinary skill in the art, such as exposing cells to a pulse of radiolabeled thymidine and measuring the incorporation of label into cellular DNA. In general, a polypeptide that
20 results in at least a three fold increase in proliferation above background (*i.e.*, the proliferation observed for cells cultured without polypeptide) is considered to be able to induce proliferation.

The ability of a polypeptide to stimulate the production of interferon- γ and/or interleukin-12 in cells may be evaluated by contacting the cells with the
25 polypeptide and measuring the level of interferon- γ or interleukin-12 produced by the cells. In general, the amount of polypeptide that is sufficient for the evaluation of about 10^5 cells ranges from about 10 ng/mL to about 100 μ g/mL and preferably is about 10 μ g/mL. The polypeptide may, but need not, be immobilized on a solid support, such as a bead or a biodegradable microsphere, such as those described in U.S. Patent
30 Nos. 4,897,268 and 5,075,109. The incubation of polypeptide with the cells is typically

performed at 37°C for about six days. Following incubation with polypeptide, the cells are assayed for interferon- γ and/or interleukin-12 (or one or more subunits thereof), which may be evaluated by methods known to those of ordinary skill in the art, such as an enzyme-linked immunosorbent assay (ELISA) or, in the case of IL-12 P70 subunit, a
5 bioassay such as an assay measuring proliferation of T cells. In general, a polypeptide that results in the production of at least 50 pg of interferon- γ per mL of cultured supernatant (containing 10^4 - 10^5 T cells per mL) is considered able to stimulate the production of interferon- γ . A polypeptide that stimulates the production of at least 10 pg/mL of IL-12 P70 subunit, and/or at least 100 pg/mL of IL-12 P40 subunit, per 10^5
10 macrophages or B cells (or per 3×10^5 PBMC) is considered able to stimulate the production of IL-12.

In general, immunogenic antigens are those antigens that stimulate proliferation and/or cytokine production (*i.e.*, interferon- γ and/or interleukin-12 production) in T cells, NK cells, B cells and/or macrophages derived from at least about
15 25% of *M. tuberculosis*-immune individuals. Among these immunogenic antigens, polypeptides having superior therapeutic properties may be distinguished based on the magnitude of the responses in the above assays and based on the percentage of individuals for which a response is observed. In addition, antigens having superior therapeutic properties will not stimulate proliferation and/or cytokine production *in*
20 *vitro* in cells derived from more than about 25% of individuals that are not *M. tuberculosis*-immune, thereby eliminating responses that are not specifically due to *M. tuberculosis*-responsive cells. Those antigens that induce a response in a high percentage of T cell, NK cell, B cell and/or macrophage preparations from *M. tuberculosis*-immune individuals (with a low incidence of responses in cell
25 preparations from other individuals) have superior therapeutic properties.

Antigens with superior therapeutic properties may also be identified based on their ability to diminish the severity of *M. tuberculosis* infection in experimental animals, when administered as a vaccine. Suitable vaccine preparations for use on experimental animals are described in detail below. Efficacy may be
30 determined based on the ability of the antigen to provide at least about a 50% reduction

in bacterial numbers and/or at least about a 40% decrease in mortality following experimental infection. Suitable experimental animals include mice, guinea pigs and primates.

Antigens having superior diagnostic properties may generally be
5 identified based on the ability to elicit a response in an intradermal skin test performed on an individual with active tuberculosis, but not in a test performed on an individual who is not infected with *M. tuberculosis*. Skin tests may generally be performed as described below, with a response of at least 5 mm induration considered positive.

Immunogenic portions of the antigens described herein may be prepared
10 and identified using well known techniques, such as those summarized in Paul, *Fundamental Immunology*, 3d ed., Raven Press, 1993, pp. 243-247 and references cited therein. Such techniques include screening polypeptide portions of the native antigen for immunogenic properties. The representative proliferation and cytokine production assays described herein may generally be employed in these screens. An immunogenic
15 portion of a polypeptide is a portion that, within such representative assays, generates an immune response (e.g., proliferation, interferon- γ production and/or interleukin-12 production) that is substantially similar to that generated by the full length antigen. In other words, an immunogenic portion of an antigen may generate at least about 20%, and preferably about 100%, of the proliferation induced by the full length antigen in the
20 model proliferation assay described herein. An immunogenic portion may also, or alternatively, stimulate the production of at least about 20%, and preferably about 100%, of the interferon- γ and/or interleukin-12 induced by the full length antigen in the model assay described herein.

Portions and other variants of *M. tuberculosis* antigens may be generated
25 by synthetic or recombinant means. Synthetic polypeptides having fewer than about 100 amino acids, and generally fewer than about 50 amino acids, may be generated using techniques well known to those of ordinary skill in the art. For example, such polypeptides may be synthesized using any of the commercially available solid-phase techniques, such as the Merrifield solid-phase synthesis method, where amino acids are
30 sequentially added to a growing amino acid chain. See Merrifield, *J. Am. Chem. Soc.*

85:2149-2146, 1963. Equipment for automated synthesis of polypeptides is commercially available from suppliers such as Applied BioSystems, Inc., Foster City, CA, and may be operated according to the manufacturer's instructions. Variants of a native antigen may generally be prepared using standard mutagenesis techniques, such as oligonucleotide-directed site-specific mutagenesis. Sections of the DNA sequence may also be removed using standard techniques to permit preparation of truncated polypeptides.

Recombinant polypeptides containing portions and/or variants of a native antigen may be readily prepared from a DNA sequence encoding the polypeptide using a variety of techniques well known to those of ordinary skill in the art. For example, supernatants from suitable host/vector systems which secrete recombinant protein into culture media may be first concentrated using a commercially available filter. Following concentration, the concentrate may be applied to a suitable purification matrix such as an affinity matrix or an ion exchange resin. Finally, one or more reverse phase HPLC steps can be employed to further purify a recombinant protein.

Any of a variety of expression vectors known to those of ordinary skill in the art may be employed to express recombinant polypeptides of this invention. Expression may be achieved in any appropriate host cell that has been transformed or transfected with an expression vector containing a DNA molecule that encodes a recombinant polypeptide. Suitable host cells include prokaryotes, yeast and higher eukaryotic cells. Preferably, the host cells employed are *E. coli*, yeast or a mammalian cell line such as COS or CHO. The DNA sequences expressed in this manner may encode naturally occurring antigens, portions of naturally occurring antigens, or other variants thereof.

In general, regardless of the method of preparation, the polypeptides disclosed herein are prepared in substantially pure form. Preferably, the polypeptides are at least about 80% pure, more preferably at least about 90% pure and most preferably at least about 99% pure. In certain preferred embodiments, described in

detail below, the substantially pure polypeptides are incorporated into pharmaceutical compositions or vaccines for use in one or more of the methods disclosed herein.

In certain specific embodiments, the subject invention discloses polypeptides comprising at least an immunogenic portion of a soluble *M. tuberculosis* antigen having one of the following N-terminal sequences, or a variant thereof that
5 differs only in conservative substitutions and/or modifications:

- (a) Asp-Pro-Val-Asp-Ala-Val-Ile-Asn-Thr-Thr-Cys-Asn-Tyr-Gly-Gln-Val-Val-Ala-Ala-Leu; (SEQ ID No. 120)
- (b) Ala-Val-Glu-Ser-Gly-Met-Leu-Ala-Leu-Gly-Thr-Pro-Ala-Pro-Ser; (SEQ ID No. 121)
10
- (c) Ala-Ala-Met-Lys-Pro-Arg-Thr-Gly-Asp-Gly-Pro-Leu-Glu-Ala-Ala-Lys-Glu-Gly-Arg; (SEQ ID No. 122)
- (d) Tyr-Tyr-Trp-Cys-Pro-Gly-Gln-Pro-Phe-Asp-Pro-Ala-Trp-Gly-Pro; (SEQ ID No. 123)
- (e) Asp-Ile-Gly-Ser-Glu-Ser-Thr-Glu-Asp-Gln-Gln-Xaa-Ala-Val; (SEQ ID No. 124)
15
- (f) Ala-Glu-Glu-Ser-Ile-Ser-Thr-Xaa-Glu-Xaa-Ile-Val-Pro; (SEQ ID No. 125)
- (g) Asp-Pro-Glu-Pro-Ala-Pro-Pro-Val-Pro-Thr-Ala-Ala-Ala-Ser-Pro-Pro-Ser; (SEQ ID No. 126)
20
- (h) Ala-Pro-Lys-Thr-Tyr-Xaa-Glu-Glu-Leu-Lys-Gly-Thr-Asp-Thr-Gly; (SEQ ID No. 127)
- (i) Asp-Pro-Ala-Ser-Ala-Pro-Asp-Val-Pro-Thr-Ala-Ala-Gln-Leu-Thr-Ser-Leu-Leu-Asn-Ser-Leu-Ala-Asp-Pro-Asn-Val-Ser-Phe-Ala-Asn; (SEQ ID No. 128)
25
- (j) Xaa-Asp-Ser-Glu-Lys-Ser-Ala-Thr-Ile-Lys-Val-Thr-Asp-Ala-Ser; (SEQ ID No. 134)
- (k) Ala-Gly-Asp-Thr-Xaa-Ile-Tyr-Ile-Val-Gly-Asn-Leu-Thr-Ala-Asp; (SEQ ID No. 135) or

- (l) Ala-Pro-Glu-Ser-Gly-Ala-Gly-Leu-Gly-Gly-Thr-Val-Gln-Ala-Gly; (SEQ ID No. 136)

wherein Xaa may be any amino acid, preferably a cysteine residue. A DNA sequence encoding the antigen identified as (g) above is provided in SEQ ID No. 52, and the polypeptide encoded by SEQ ID No. 52 is provided in SEQ ID No. 53. A DNA sequence encoding the antigen defined as (a) above is provided in SEQ ID No. 101; its deduced amino acid sequence is provided in SEQ ID No. 102. A DNA sequence corresponding to antigen (d) above is provided in SEQ ID No. 24 a DNA sequence corresponding to antigen (c) is provided in SEQ ID No. 25 and a DNA sequence corresponding to antigen (i) is provided in SEQ ID No. 99; its deduced amino acid sequence is provided in SEQ ID No. 100.

In a further specific embodiment, the subject invention discloses polypeptides comprising at least an immunogenic portion of an *M. tuberculosis* antigen having one of the following N-terminal sequences, or a variant thereof that differs only in conservative substitutions and/or modifications:

- (m) Xaa-Tyr-Ile-Ala-Tyr-Xaa-Thr-Thr-Ala-Gly-Ile-Val-Pro-Gly-Lys-Ile-Asn-Val-His-Leu-Val; (SEQ ID No 137) or

- (n) Asp-Pro-Pro-Asp-Pro-His-Gln-Xaa-Asp-Met-Thr-Lys-Gly-Tyr-Tyr-Pro-Gly-Gly-Arg-Arg-Xaa-Phe; (SEQ ID No. 129)

wherein Xaa may be any amino acid, preferably a cysteine residue.

In other specific embodiments, the subject invention discloses polypeptides comprising at least an immunogenic portion of a soluble *M. tuberculosis* antigen (or a variant of such an antigen) that comprises one or more of the amino acid sequences encoded by (a) the DNA sequences of SEQ ID Nos.: 1, 2, 4-10, 13-25 and 52; (b) the complements of such DNA sequences, or (c) DNA sequences substantially homologous to a sequence in (a) or (b).

In further specific embodiments, the subject invention discloses polypeptides comprising at least an immunogenic portion of a *M. tuberculosis* antigen (or a variant of such an antigen), which may or may not be soluble, that comprises one or more of the amino acid sequences encoded by (a) the DNA sequences of SEQ ID

Nos.: 26-51, 138, 139, 163-183 and 201, (b) the complements of such DNA sequences or (c) DNA sequences substantially homologous to a sequence in (a) or (b).

In the specific embodiments discussed above, the *M. tuberculosis* antigens include variants that are encoded by DNA sequences which are substantially
5 homologous to one or more of DNA sequences specifically recited herein. "Substantial homology," as used herein, refers to DNA sequences that are capable of hybridizing under moderately stringent conditions. Suitable moderately stringent conditions include prewashing in a solution of 5X SSC, 0.5% SDS, 1.0 mM EDTA (pH 8.0); hybridizing at 50°C-65°C, 5X SSC, overnight or, in the case of cross-species homology at 45°C,
10 0.5X SSC; followed by washing twice at 65°C for 20 minutes with each of 2X, 0.5X and 0.2X SSC containing 0.1% SDS). Such hybridizing DNA sequences are also within the scope of this invention, as are nucleotide sequences that, due to code degeneracy, encode an immunogenic polypeptide that is encoded by a hybridizing DNA sequence.

15 In a related aspect, the present invention provides fusion proteins comprising a first and a second inventive polypeptide or, alternatively, a polypeptide of the present invention and a known *M. tuberculosis* antigen, such as the 38 kD antigen described in Andersen and Hansen, *Infect. Immun.* 57:2481-2488, 1989, (Genbank Accession No. M30046) or ESAT-6 (SEQ ID Nos. 103 and 104), together with variants
20 of such fusion proteins. The fusion proteins of the present invention may also include a linker peptide between the first and second polypeptides.

A DNA sequence encoding a fusion protein of the present invention is constructed using known recombinant DNA techniques to assemble separate DNA sequences encoding the first and second polypeptides into an appropriate expression
25 vector. The 3' end of a DNA sequence encoding the first polypeptide is ligated, with or without a peptide linker, to the 5' end of a DNA sequence encoding the second polypeptide so that the reading frames of the sequences are in phase to permit mRNA translation of the two DNA sequences into a single fusion protein that retains the biological activity of both the first and the second polypeptides.

A peptide linker sequence may be employed to separate the first and the second polypeptides by a distance sufficient to ensure that each polypeptide folds into its secondary and tertiary structures. Such a peptide linker sequence is incorporated into the fusion protein using standard techniques well known in the art. Suitable peptide linker sequences may be chosen based on the following factors: (1) their ability to adopt a flexible extended conformation; (2) their inability to adopt a secondary structure that could interact with functional epitopes on the first and second polypeptides; and (3) the lack of hydrophobic or charged residues that might react with the polypeptide functional epitopes. Preferred peptide linker sequences contain Gly, Asn and Ser residues. Other near neutral amino acids, such as Thr and Ala may also be used in the linker sequence. Amino acid sequences which may be usefully employed as linkers include those disclosed in Maratea et al., *Gene* 40:39-46, 1985; Murphy et al., *Proc. Natl. Acad. Sci. USA* 83:8258-8262, 1986; U.S. Patent No. 4,935,233 and U.S. Patent No. 4,751,180. The linker sequence may be from 1 to about 50 amino acids in length. Peptide sequences are not required when the first and second polypeptides have non-essential N-terminal amino acid regions that can be used to separate the functional domains and prevent steric interference.

The ligated DNA sequences are operably linked to suitable transcriptional or translational regulatory elements. The regulatory elements responsible for expression of DNA are located only 5' to the DNA sequence encoding the first polypeptides. Similarly, stop codons require to end translation and transcription termination signals are only present 3' to the DNA sequence encoding the second polypeptide.

In another aspect, the present invention provides methods for using one or more of the above polypeptides or fusion proteins (or DNA molecules encoding such polypeptides) to induce protective immunity against tuberculosis in a patient. As used herein, a "patient" refers to any warm-blooded animal, preferably a human. A patient may be afflicted with a disease, or may be free of detectable disease and/or infection. In other words, protective immunity may be induced to prevent or treat tuberculosis.

In this aspect, the polypeptide, fusion protein or DNA molecule is generally present within a pharmaceutical composition and/or a vaccine. Pharmaceutical compositions may comprise one or more polypeptides, each of which may contain one or more of the above sequences (or variants thereof), and a
5 physiologically acceptable carrier. Vaccines may comprise one or more of the above polypeptides and a non-specific immune response enhancer, such as an adjuvant or a liposome (into which the polypeptide is incorporated). Such pharmaceutical compositions and vaccines may also contain other *M. tuberculosis* antigens, either incorporated into a combination polypeptide or present within a separate polypeptide.

10 Alternatively, a vaccine may contain DNA encoding one or more polypeptides as described above, such that the polypeptide is generated *in situ*. In such vaccines, the DNA may be present within any of a variety of delivery systems known to those of ordinary skill in the art, including nucleic acid expression systems, bacterial and viral expression systems. Appropriate nucleic acid expression systems contain the
15 necessary DNA sequences for expression in the patient (such as a suitable promoter and terminating signal). Bacterial delivery systems involve the administration of a bacterium (such as *Bacillus-Calmette-Guerrin*) that expresses an immunogenic portion of the polypeptide on its cell surface. In a preferred embodiment, the DNA may be introduced using a viral expression system (*e.g.*, vaccinia or other pox virus, retrovirus,
20 or adenovirus), which may involve the use of a non-pathogenic (defective), replication competent virus. Techniques for incorporating DNA into such expression systems are well known to those of ordinary skill in the art. The DNA may also be "naked," as described, for example, in Ulmer et al., *Science* 259:1745-1749, 1993 and reviewed by Cohen, *Science* 259:1691-1692, 1993. The uptake of naked DNA may be increased by
25 coating the DNA onto biodegradable beads, which are efficiently transported into the cells.

In a related aspect, a DNA vaccine as described above may be administered simultaneously with or sequentially to either a polypeptide of the present invention or a known *M. tuberculosis* antigen, such as the 38 kD antigen described
30 above. For example, administration of DNA encoding a polypeptide of the present

invention, either "naked" or in a delivery system as described above, may be followed by administration of an antigen in order to enhance the protective immune effect of the vaccine.

Routes and frequency of administration, as well as dosage, will vary from individual to individual and may parallel those currently being used in immunization using BCG. In general, the pharmaceutical compositions and vaccines may be administered by injection (*e.g.*, intracutaneous, intramuscular, intravenous or subcutaneous), intranasally (*e.g.*, by aspiration) or orally. Between 1 and 3 doses may be administered for a 1-36 week period. Preferably, 3 doses are administered, at intervals of 3-4 months, and booster vaccinations may be given periodically thereafter. Alternate protocols may be appropriate for individual patients. A suitable dose is an amount of polypeptide or DNA that, when administered as described above, is capable of raising an immune response in an immunized patient sufficient to protect the patient from *M. tuberculosis* infection for at least 1-2 years. In general, the amount of polypeptide present in a dose (or produced *in situ* by the DNA in a dose) ranges from about 1 pg to about 100 mg per kg of host, typically from about 10 pg to about 1 mg, and preferably from about 100 pg to about 1 μ g. Suitable dose sizes will vary with the size of the patient, but will typically range from about 0.1 mL to about 5 mL.

While any suitable carrier known to those of ordinary skill in the art may be employed in the pharmaceutical compositions of this invention, the type of carrier will vary depending on the mode of administration. For parenteral administration, such as subcutaneous injection, the carrier preferably comprises water, saline, alcohol, a fat, a wax or a buffer. For oral administration, any of the above carriers or a solid carrier, such as mannitol, lactose, starch, magnesium stearate, sodium saccharine, talcum, cellulose, glucose, sucrose, and magnesium carbonate, may be employed. Biodegradable microspheres (*e.g.*, polylactic galactide) may also be employed as carriers for the pharmaceutical compositions of this invention. Suitable biodegradable microspheres are disclosed, for example, in U.S. Patent Nos. 4,897,268 and 5,075,109.

Any of a variety of adjuvants may be employed in the vaccines of this invention to nonspecifically enhance the immune response. Most adjuvants contain a

substance designed to protect the antigen from rapid catabolism, such as aluminum hydroxide or mineral oil, and a nonspecific stimulator of immune responses, such as lipid A, *Bordetella pertussis* or *Mycobacterium tuberculosis*. Suitable adjuvants are commercially available as, for example, Freund's Incomplete Adjuvant and Freund's
5 Complete Adjuvant (Difco Laboratories) and Merck Adjuvant 65 (Merck and Company, Inc., Rahway, NJ). Other suitable adjuvants include alum, biodegradable microspheres, monophosphoryl lipid A and quil A.

In another aspect, this invention provides methods for using one or more of the polypeptides described above to diagnose tuberculosis using a skin test. As used
10 herein, a "skin test" is any assay performed directly on a patient in which a delayed-type hypersensitivity (DTH) reaction (such as swelling, reddening or dermatitis) is measured following intradermal injection of one or more polypeptides as described above. Such injection may be achieved using any suitable device sufficient to contact the polypeptide or polypeptides with dermal cells of the patient, such as a tuberculin
15 syringe or 1 mL syringe. Preferably, the reaction is measured at least 48 hours after injection, more preferably 48-72 hours.

The DTH reaction is a cell-mediated immune response, which is greater in patients that have been exposed previously to the test antigen (*i.e.*, the immunogenic portion of the polypeptide employed, or a variant thereof). The response may be
20 measured visually, using a ruler. In general, a response that is greater than about 0.5 cm in diameter, preferably greater than about 1.0 cm in diameter, is a positive response, indicative of tuberculosis infection, which may or may not be manifested as an active disease.

The polypeptides of this invention are preferably formulated, for use in a
25 skin test, as pharmaceutical compositions containing a polypeptide and a physiologically acceptable carrier, as described above. Such compositions typically contain one or more of the above polypeptides in an amount ranging from about 1 μ g to about 100 μ g, preferably from about 10 μ g to about 50 μ g in a volume of 0.1 mL. Preferably, the carrier employed in such pharmaceutical compositions is a saline
30 solution with appropriate preservatives, such as phenol and/or Tween 80™.

In a preferred embodiment, a polypeptide employed in a skin test is of sufficient size such that it remains at the site of injection for the duration of the reaction period. In general, a polypeptide that is at least 9 amino acids in length is sufficient. The polypeptide is also preferably broken down by macrophages within hours of
5 injection to allow presentation to T-cells. Such polypeptides may contain repeats of one or more of the above sequences and/or other immunogenic or nonimmunogenic sequences.

The following Examples are offered by way of illustration and not by
10 way of limitation.

EXAMPLES

EXAMPLE 1

PURIFICATION AND CHARACTERIZATION OF POLYPEPTIDES FROM *M. TUBERCULOSIS* CULTURE FILTRATE

This example illustrates the preparation of *M. tuberculosis* soluble polypeptides from culture filtrate. Unless otherwise noted, all percentages in the
20 following example are weight per volume.

M. tuberculosis (either H37Ra, ATCC No. 25177, or H37Rv, ATCC No. 25618) was cultured in sterile GAS media at 37°C for fourteen days. The media was then vacuum filtered (leaving the bulk of the cells) through a 0.45 µ filter into a sterile 2.5 L bottle. The media was next filtered through a 0.2 µ filter into a sterile 4 L
25 bottle and NaN₃ was added to the culture filtrate to a concentration of 0.04%. The bottles were then placed in a 4°C cold room.

The culture filtrate was concentrated by placing the filtrate in a 12 L reservoir that had been autoclaved and feeding the filtrate into a 400 ml Amicon stir cell which had been rinsed with ethanol and contained a 10,000 kDa MWCO membrane.

The pressure was maintained at 60 psi using nitrogen gas. This procedure reduced the 12 L volume to approximately 50 ml.

The culture filtrate was dialyzed into 0.1% ammonium bicarbonate using a 8,000 kDa MWCO cellulose ester membrane, with two changes of ammonium
5 bicarbonate solution. Protein concentration was then determined by a commercially available BCA assay (Pierce, Rockford, IL).

The dialyzed culture filtrate was then lyophilized, and the polypeptides resuspended in distilled water. The polypeptides were dialyzed against 0.01 mM 1,3 bis[tris(hydroxymethyl)-methylamino]propane, pH 7.5 (Bis-Tris propane buffer), the
10 initial conditions for anion exchange chromatography. Fractionation was performed using gel perfusion chromatography on a POROS 146 II Q/M anion exchange column 4.6 mm x 100 mm (Perseptive BioSystems, Framingham, MA) equilibrated in 0.01 mM Bis-Tris propane buffer pH 7.5. Polypeptides were eluted with a linear 0-0.5 M NaCl gradient in the above buffer system. The column eluent was monitored at a wavelength
15 of 220 nm.

The pools of polypeptides eluting from the ion exchange column were dialyzed against distilled water and lyophilized. The resulting material was dissolved in 0.1% trifluoroacetic acid (TFA) pH 1.9 in water, and the polypeptides were purified on a Delta-Pak C18 column (Waters, Milford, MA) 300 Angstrom pore size, 5 micron
20 particle size (3.9 x 150 mm). The polypeptides were eluted from the column with a linear gradient from 0-60% dilution buffer (0.1% TFA in acetonitrile). The flow rate was 0.75 ml/minute and the HPLC eluent was monitored at 214 nm. Fractions containing the eluted polypeptides were collected to maximize the purity of the individual samples. Approximately 200 purified polypeptides were obtained.

25 The purified polypeptides were then screened for the ability to induce T-cell proliferation in PBMC preparations. The PBMCs from donors known to be PPD skin test positive and whose T-cells were shown to proliferate in response to PPD and crude soluble proteins from MTB were cultured in medium comprising RPMI 1640 supplemented with 10% pooled human serum and 50 µg/ml gentamicin. Purified
30 polypeptides were added in duplicate at concentrations of 0.5 to 10 µg/mL. After six

days of culture in 96-well round-bottom plates in a volume of 200 μ l, 50 μ l of medium was removed from each well for determination of IFN- γ levels, as described below. The plates were then pulsed with 1 μ Ci/well of tritiated thymidine for a further 18 hours, harvested and tritium uptake determined using a gas scintillation counter.

- 5 Fractions that resulted in proliferation in both replicates three fold greater than the proliferation observed in cells cultured in medium alone were considered positive.

IFN- γ was measured using an enzyme-linked immunosorbent assay (ELISA). ELISA plates were coated with a mouse monoclonal antibody directed to human IFN- γ (PharMingen, San Diego, CA) in PBS for four hours at room temperature.

10 Wells were then blocked with PBS containing 5% (W/V) non-fat dried milk for 1 hour at room temperature. The plates were then washed six times in PBS/0.2% TWEEN-20 and samples diluted 1:2 in culture medium in the ELISA plates were incubated overnight at room temperature. The plates were again washed and a polyclonal rabbit anti-human IFN- γ serum diluted 1:3000 in PBS/10% normal goat serum was added to

15 each well. The plates were then incubated for two hours at room temperature, washed and horseradish peroxidase-coupled anti-rabbit IgG (Sigma Chemical So., St. Louis, MO) was added at a 1:2000 dilution in PBS/5% non-fat dried milk. After a further two hour incubation at room temperature, the plates were washed and TMB substrate added. The reaction was stopped after 20 min with 1 N sulfuric acid. Optical density was

20 determined at 450 nm using 570 nm as a reference wavelength. Fractions that resulted in both replicates giving an OD two fold greater than the mean OD from cells cultured in medium alone, plus 3 standard deviations, were considered positive.

For sequencing, the polypeptides were individually dried onto Biobrene™ (Perkin Elmer/Applied BioSystems Division, Foster City, CA) treated glass

25 fiber filters. The filters with polypeptide were loaded onto a Perkin Elmer/Applied BioSystems Division Procise 492 protein sequencer. The polypeptides were sequenced from the amino terminal and using traditional Edman chemistry. The amino acid sequence was determined for each polypeptide by comparing the retention time of the PTH amino acid derivative to the appropriate PTH derivative standards.

Using the procedure described above, antigens having the following N-terminal sequences were isolated:

- (a) Asp-Pro-Val-Asp-Ala-Val-Ile-Asn-Thr-Thr-Xaa-Asn-Tyr-Gly-Gln-Val-Val-Ala-Ala-Leu; (SEQ ID No. 54)
- 5 (b) Ala-Val-Glu-Ser-Gly-Met-Leu-Ala-Leu-Gly-Thr-Pro-Ala-Pro-Ser; (SEQ ID No. 55)
- (c) Ala-Ala-Met-Lys-Pro-Arg-Thr-Gly-Asp-Gly-Pro-Leu-Glu-Ala-Ala-Lys-Glu-Gly-Arg; (SEQ ID No. 56)
- (d) Tyr-Tyr-Trp-Cys-Pro-Gly-Gln-Pro-Phe-Asp-Pro-Ala-Trp-Gly-Pro; (SEQ ID No. 57)
- 10 (e) Asp-Ile-Gly-Ser-Glu-Ser-Thr-Glu-Asp-Gln-Gln-Xaa-Ala-Val; (SEQ ID No. 58)
- (f) Ala-Glu-Glu-Ser-Ile-Ser-Thr-Xaa-Glu-Xaa-Ile-Val-Pro; (SEQ ID No. 59)
- 15 (g) Asp-Pro-Glu-Pro-Ala-Pro-Pro-Val-Pro-Thr-Ala-Ala-Ala-Ala-Pro-Pro-Ala; (SEQ ID No. 60) and
- (h) Ala-Pro-Lys-Thr-Tyr-Xaa-Glu-Glu-Leu-Lys-Gly-Thr-Asp-Thr-Gly; (SEQ ID No. 61)

wherein Xaa may be any amino acid.

- 20 An additional antigen was isolated employing a microbore HPLC purification step in addition to the procedure described above. Specifically, 20 μ l of a fraction comprising a mixture of antigens from the chromatographic purification step previously described, was purified on an Aquapore C18 column (Perkin Elmer/Applied Biosystems Division, Foster City, CA) with a 7 micron pore size, column size 1 mm x
- 25 100 mm, in a Perkin Elmer/Applied Biosystems Division Model 172 HPLC. Fractions were eluted from the column with a linear gradient of 1%/minute of acetonitrile (containing 0.05% TFA) in water (0.05% TFA) at a flow rate of 80 μ l/minute. The eluent was monitored at 250 nm. The original fraction was separated into 4 major peaks plus other smaller components and a polypeptide was obtained which was shown to

have a molecular weight of 12.054 Kd (by mass spectrometry) and the following N-terminal sequence:

- (i) Asp-Pro-Ala-Ser-Ala-Pro-Asp-Val-Pro-Thr-Ala-Ala-Gln-Gln-
Thr-Ser-Leu-Leu-Asn-Asn-Leu-Ala-Asp-Pro-Asp-Val-Ser-Phe-
5 Ala-Asp (SEQ ID No. 62).

This polypeptide was shown to induce proliferation and IFN- γ production in PBMC preparations using the assays described above.

Additional soluble antigens were isolated from *M. tuberculosis* culture filtrate as follows. *M. tuberculosis* culture filtrate was prepared as described above.
10 Following dialysis against Bis-Tris propane buffer, at pH 5.5, fractionation was performed using anion exchange chromatography on a Poros QE column 4.6 x 100 mm (Perseptive Biosystems) equilibrated in Bis-Tris propane buffer pH 5.5. Polypeptides were eluted with a linear 0-1.5 M NaCl gradient in the above buffer system at a flow rate of 10 ml/min. The column eluent was monitored at a wavelength of 214 nm.

15 The fractions eluting from the ion exchange column were pooled and subjected to reverse phase chromatography using a Poros R2 column 4.6 x 100 mm (Perseptive Biosystems). Polypeptides were eluted from the column with a linear gradient from 0-100% acetonitrile (0.1% TFA) at a flow rate of 5 ml/min. The eluent was monitored at 214 nm.

20 Fractions containing the eluted polypeptides were lyophilized and resuspended in 80 μ l of aqueous 0.1% TFA and further subjected to reverse phase chromatography on a Vydac C4 column 4.6 x 150 mm (Western Analytical, Temecula, CA) with a linear gradient of 0-100% acetonitrile (0.1% TFA) at a flow rate of 2 ml/min. Eluent was monitored at 214 nm.

25 The fraction with biological activity was separated into one major peak plus other smaller components. Western blot of this peak onto PVDF membrane revealed three major bands of molecular weights 14 Kd, 20 Kd and 26 Kd. These polypeptides were determined to have the following N-terminal sequences, respectively:

- (j) Xaa-Asp-Ser-Glu-Lys-Ser-Ala-Thr-Ile-Lys-Val-Thr-Asp-Ala-
30 Ser; (SEQ ID No. 134)

- (k) Ala-Gly-Asp-Thr-Xaa-Ile-Tyr-Ile-Val-Gly-Asn-Leu-Thr-Ala-Asp; (SEQ ID No. 135) and
- (l) Ala-Pro-Glu-Ser-Gly-Ala-Gly-Leu-Gly-Gly-Thr-Val-Gln-Ala-Gly; (SEQ ID No. 136), wherein Xaa may be any amino acid.

5 Using the assays described above, these polypeptides were shown to induce proliferation and IFN- γ production in PBMC preparations. Figs. 1A and B show the results of such assays using PBMC preparations from a first and a second donor, respectively.

DNA sequences that encode the antigens designated as (a), (c), (d) and
10 (g) above were obtained by screening a genomic *M. tuberculosis* library using ^{32}P end labeled degenerate oligonucleotides corresponding to the N-terminal sequence and containing *M. tuberculosis* codon bias. The screen performed using a probe corresponding to antigen (a) above identified a clone having the sequence provided in SEQ ID No. 101. The polypeptide encoded by SEQ ID No. 101 is provided in SEQ ID
15 No. 102. The screen performed using a probe corresponding to antigen (g) above identified a clone having the sequence provided in SEQ ID No. 52. The polypeptide encoded by SEQ ID No. 52 is provided in SEQ ID No. 53. The screen performed using a probe corresponding to antigen (d) above identified a clone having the sequence provided in SEQ ID No. 24, and the screen performed with a probe corresponding to
20 antigen (c) identified a clone having the sequence provided in SEQ ID No: 25.

The above amino acid sequences were compared to known amino acid sequences in the gene bank using the DNA STAR system. The database searched contains some 173,000 proteins and is a combination of the Swiss, PIR databases along with translated protein sequences (Version 87). No significant homologies to the amino
25 acid sequences for antigens (a)-(h) and (l) were detected.

The amino acid sequence for antigen (i) was found to be homologous to a sequence from *M. leprae*. The full length *M. leprae* sequence was amplified from genomic DNA using the sequence obtained from GENBANK. This sequence was then used to screen the *M. tuberculosis* library described below in Example 2 and a full
30 length copy of the *M. tuberculosis* homologue was obtained (SEQ ID No. 99).

The amino acid sequence for antigen (j) was found to be homologous to a known *M. tuberculosis* protein translated from a DNA sequence. To the best of the inventors' knowledge, this protein has not been previously shown to possess T-cell stimulatory activity. The amino acid sequence for antigen (k) was found to be related to
 5 a sequence from *M. leprae*.

In the proliferation and IFN- γ assays described above, using three PPD positive donors, the results for representative antigens provided above are presented in Table 1:

10

TABLE 1RESULTS OF PBMC PROLIFERATION AND IFN- γ ASSAYS

Sequence	Proliferation	IFN- γ
(a)	+	-
(c)	+++	+++
(d)	++	++
(g)	+++	+++
(h)	+++	+++

In Table 1, responses that gave a stimulation index (SI) of between 2 and
 15 4 (compared to cells cultured in medium alone) were scored as +, an SI of 4-8 or 2-4 at a concentration of 1 μ g or less was scored as ++ and an SI of greater than 8 was scored as +++. The antigen of sequence (i) was found to have a high SI (+++) for one donor and lower SI (++ and +) for the two other donors in both proliferation and IFN- γ assays. These results indicate that these antigens are capable of inducing proliferation and/or
 20 interferon- γ production.

EXAMPLE 2USE OF PATIENT SERA TO ISOLATE *M. TUBERCULOSIS* ANTIGENS

This example illustrates the isolation of antigens from *M. tuberculosis* lysate by screening with serum from *M. tuberculosis*-infected individuals.

Dessicated *M. tuberculosis* H37Ra (Difco Laboratories) was added to a 2% NP40 solution, and alternately homogenized and sonicated three times. The resulting suspension was centrifuged at 13,000 rpm in microfuge tubes and the supernatant put through a 0.2 micron syringe filter. The filtrate was bound to Macro Prep DEAE beads (BioRad, Hercules, CA). The beads were extensively washed with 20 mM Tris pH 7.5 and bound proteins eluted with 1M NaCl. The 1M NaCl elute was dialyzed overnight against 10 mM Tris, pH 7.5. Dialyzed solution was treated with DNase and RNase at 0.05 mg/ml for 30 min. at room temperature and then with α -D-mannosidase, 0.5 U/mg at pH 4.5 for 3-4 hours at room temperature. After returning to pH 7.5, the material was fractionated via FPLC over a Bio Scale-Q-20 column (BioRad). Fractions were combined into nine pools, concentrated in a Centriprep 10 (Amicon, Beverley, MA) and then screened by Western blot for serological activity using a serum pool from *M. tuberculosis*-infected patients which was not immunoreactive with other antigens of the present invention.

The most reactive fraction was run in SDS-PAGE and transferred to PVDF. A band at approximately 85 Kd was cut out yielding the sequence:

(m) Xaa-Tyr-Ile-Ala-Tyr-Xaa-Thr-Thr-Ala-Gly-Ile-Val-Pro-Gly-Lys-Ile-Asn-Val-His-Leu-Val; (SEQ ID No. 137), wherein Xaa may be any amino acid.

Comparison of this sequence with those in the gene bank as described above, revealed no significant homologies to known sequences.

A DNA sequence that encodes the antigen designated as (m) above was obtained by screening a genomic *M. tuberculosis* Erdman strain library using labeled degenerate oligonucleotides corresponding to the N-terminal sequence of SEQ ID NO:137. A clone was identified having the DNA sequence provided in SEQ ID NO:

203. This sequence was found to encode the amino acid sequence provided in SEQ ID NO: 204. Comparison of these sequences with those in the genebank revealed some similarity to sequences previously identified in *M. tuberculosis* and *M. bovis*.

5

EXAMPLE 3

PREPARATION OF DNA SEQUENCES ENCODING *M. TUBERCULOSIS* ANTIGENS

This example illustrates the preparation of DNA sequences encoding *M. tuberculosis* antigens by screening a *M. tuberculosis* expression library with sera
10 obtained from patients infected with *M. tuberculosis*, or with anti-sera raised against soluble *M. tuberculosis* antigens.

A. PREPARATION OF *M. TUBERCULOSIS* SOLUBLE ANTIGENS USING RABBIT ANTI-SERA RAISED AGAINST *M. TUBERCULOSIS* SUPERNATANT

15 Genomic DNA was isolated from the *M. tuberculosis* strain H37Ra. The DNA was randomly sheared and used to construct an expression library using the Lambda ZAP expression system (Stratagene, La Jolla, CA). Rabbit anti-sera was generated against secretory proteins of the *M. tuberculosis* strains H37Ra, H37Rv and Erdman by immunizing a rabbit with concentrated supernatant of the *M. tuberculosis*
20 cultures. Specifically, the rabbit was first immunized subcutaneously with 200 µg of protein antigen in a total volume of 2 ml containing 10 µg muramyl dipeptide (Calbiochem, La Jolla, CA) and 1 ml of incomplete Freund's adjuvant. Four weeks later the rabbit was boosted subcutaneously with 100 µg antigen in incomplete Freund's adjuvant. Finally, the rabbit was immunized intravenously four weeks later with 50 µg
25 protein antigen. The anti-sera were used to screen the expression library as described in Sambrook et al., *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratories, Cold Spring Harbor, NY, 1989. Bacteriophage plaques expressing immunoreactive antigens were purified. Phagemid from the plaques was rescued and the nucleotide sequences of the *M. tuberculosis* clones deduced.

30 Thirty two clones were purified. Of these, 25 represent sequences that have not been previously identified in human *M. tuberculosis*. Recombinant antigens

were expressed and purified antigens used in the immunological analysis described in Example 1. Proteins were induced by IPTG and purified by gel elution, as described in Skeiky et al., *J. Exp. Med.* 181:1527-1537, 1995. Representative sequences of DNA molecules identified in this screen are provided in SEQ ID Nos.: 1-25. The
5 corresponding predicted amino acid sequences are shown in SEQ ID Nos. 63-87.

On comparison of these sequences with known sequences in the gene bank using the databases described above, it was found that the clones referred to hereinafter as TbRA2A, TbRA16, TbRA18, and TbRA29 (SEQ ID Nos. 76, 68, 70, 75) show some homology to sequences previously identified in *Mycobacterium leprae* but
10 not in *M. tuberculosis*. TbRA11, TbRA26, TbRA28 and TbDPEP (SEQ ID Nos.: 65, 73, 74, 53) have been previously identified in *M. tuberculosis*. No significant homologies were found to TbRA1, TbRA3, TbRA4, TbRA9, TbRA10, TbRA13, TbRA17, TbRa19, TbRA29, TbRA32, TbRA36 and the overlapping clones TbRA35 and TbRA12 (SEQ ID Nos. 63, 77, 81, 82, 64, 67, 69, 71, 75, 78, 80, 79, 66). The
15 clone TbRa24 is overlapping with clone TbRa29.

The results of PBMC proliferation and interferon- γ assays performed on representative recombinant antigens, and using T-cell preparations from several different *M. tuberculosis*-immune patients, are presented in Tables 2 and 3, respectively.

TABLE 2
RESULTS OF PBMC PROLIFERATION TO REPRESENTATIVE SOLUBLE ANTIGENS

Antigen	Patient												
	1	2	3	4	5	6	7	8	9	10	11	12	13
TbRa1	-	-	±	++	-	-	±	±	-	-	+	±	-
TbRa3	-	±	++	-	±	-	-	++	±	-	-	-	-
TbRa9	-	-	nt	nt	++	++	nt	nt	nt	nt	nt	nt	nt
TbRa10	-	-	±	±	±	+	nt	±	-	+	±	±	-
TbRa11	±	±	+	++	++	+	nt	-	++	++	++	±	nt
TbRa12	-	-	+	+	±	++	+	±	±	-	+	-	-
TbRa16	nt	nt	nt	nt	-	+	nt	nt	nt	nt	nt	nt	nt
TbRa24	nt	nt	nt	nt	-	-	nt	nt	nt	nt	nt	nt	nt
TbRa26	-	+	nt	nt	-	-	nt	nt	nt	nt	nt	nt	nt
TbRa29	nt	nt	nt	nt	-	-	nt	nt	nt	nt	nt	nt	nt
TbRa35	++	nt	++	++	++	++	nt	++	++	++	++	++	nt
TbRaB	nt	nt	nt	nt	-	-	nt	nt	nt	nt	nt	nt	nt
TbRaC	nt	nt	nt	nt	-	-	nt	nt	nt	nt	nt	nt	nt
TbRaD	nt	nt	nt	nt	-	-	nt	nt	nt	nt	nt	nt	nt
AAMK	-	-	±	-	-	-	nt	-	-	-	nt	±	nt
YY	-	-	-	-	-	-	nt	-	-	-	nt	+	nt
DPEP	-	+	-	++	-	-	nt	++	±	+	±	±	nt
Control	-	-	-	-	-	-	-	-	-	-	-	-	-

nt = not tested

TABLE 3
RESULTS OF PBMC INTERFERON- γ PRODUCTION TO REPRESENTATIVE SOLUBLE ANTIGENS

[illegible]

In Tables 2 and 3, responses that gave a stimulation index (SI) of between 1.2 and 2 (compared to cells cultured in medium alone) were scored as \pm , a SI of 2-4 was scored as +, as SI of 4-8 or 2-4 at a concentration of 1 μ g or less was scored as ++ and an SI of greater than 8 was scored as +++.

5 In addition, the effect of concentration on proliferation and interferon- γ production is shown for two of the above antigens in the attached Figure. For both proliferation and interferon- γ production, TbRa3 was scored as ++ and TbRa9 as +.

These results indicate that these soluble antigens can induce proliferation and/or interferon- γ production in T-cells derived from an *M. tuberculosis*-immune

10 individual.

B. USE OF SERA FROM PATIENTS HAVING PULMONARY OR PLEURAL TUBERCULOSIS TO IDENTIFY DNA SEQUENCES ENCODING *M. TUBERCULOSIS* ANTIGENS

The genomic DNA library described above, and an additional H37Rv

15 library, were screened using pools of sera obtained from patients with active tuberculosis. To prepare the H37Rv library, *M. tuberculosis* strain H37Rv genomic DNA was isolated, subjected to partial *Sau*3A digestion and used to construct an expression library using the Lambda Zap expression system (Stratagene, La Jolla, Ca). Three different pools of sera, each containing sera obtained from three individuals with

20 active pulmonary or pleural disease, were used in the expression screening. The pools were designated TbL, TbM and TbH, referring to relative reactivity with H37Ra lysate (*i.e.*, TbL = low reactivity, TbM = medium reactivity and TbH = high reactivity) in both ELISA and immunoblot format. A fourth pool of sera from seven patients with active pulmonary tuberculosis was also employed. All of the sera lacked increased reactivity

25 with the recombinant 38 kD *M. tuberculosis* H37Ra phosphate-binding protein.

All pools were pre-adsorbed with *E. coli* lysate and used to screen the H37Ra and H37Rv expression libraries, as described in Sambrook et al., *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratories, Cold Spring Harbor, NY, 1989. Bacteriophage plaques expressing immunoreactive antigens were purified.

30 Phagemid from the plaques was rescued and the nucleotide sequences of the *M. tuberculosis* clones deduced.

Thirty two clones were purified. Of these, 31 represented sequences that had not been previously identified in human *M. tuberculosis*. Representative sequences of the DNA molecules identified are provided in SEQ ID Nos.: 26-51 and 105. Of these, TbH-8-2 (SEQ. ID NO. 105) is a partial clone of TbH-8, and TbH-4 (SEQ. ID NO. 43) and TbH-4-FWD (SEQ. ID NO. 44) are non-contiguous sequences from the same clone. Amino acid sequences for the antigens hereinafter identified as Tb38-1, TbH-4, TbH-8, TbH-9, and TbH-12 are shown in SEQ ID Nos.: 88-92. Comparison of these sequences with known sequences in the gene bank using the databases identified above revealed no significant homologies to TbH-4, TbH-8, TbH-9 and TbM-3, although weak homologies were found to TbH-9. TbH-12 was found to be homologous to a 34 kD antigenic protein previously identified in *M. paratuberculosis* (Acc. No. S28515). Tb38-1 was found to be located 34 base pairs upstream of the open reading frame for the antigen ESAT-6 previously identified in *M. bovis* (Acc. No. U34848) and in *M. tuberculosis* (Sorensen et al., *Infec. Immun.* 63:1710-1717, 1995).

Probes derived from Tb38-1 and TbH-9, both isolated from an H37Ra library, were used to identify clones in an H37Rv library. Tb38-1 hybridized to Tb38-1F2, Tb38-1F3, Tb38-1F5 and Tb38-1F6 (SEQ. ID NOS. 112, 113, 116, 118, and 119). (SEQ ID NOS. 112 and 113 are non-contiguous sequences from clone Tb38-1F2.) Two open reading frames were deduced in Tb38-1F2; one corresponds to Tb37FL (SEQ. ID. NO. 114), the second, a partial sequence, may be the homologue of Tb38-1 and is called Tb38-IN (SEQ. ID NO. 115). The deduced amino acid sequence of Tb38-1F3 is presented in SEQ. ID. NO. 117. A TbH-9 probe identified three clones in the H37Rv library: TbH-9-FL (SEQ. ID NO. 106), which may be the homologue of TbH-9 (R37Ra), TbH-9-1 (SEQ. ID NO. 108), and TbH-9-4 (SEQ. ID NO. 110), all of which are highly related sequences to TbH-9. The deduced amino acid sequences for these three clones are presented in SEQ ID NOS. 107, 109 and 111.

Further screening of the *M. tuberculosis* genomic DNA library, as described above, resulted in the recovery of ten additional reactive clones, representing seven different genes. One of these genes was identified as the 38 Kd antigen discussed

above, one was determined to be identical to the 14Kd alpha crystallin heat shock protein previously shown to be present in *M. tuberculosis*, and a third was determined to be identical to the antigen TbH-8 described above. The determined DNA sequences for the remaining five clones (hereinafter referred to as TbH-29, TbH-30, TbH-32 and
5 TbH-33) are provided in SEQ ID NO: 138-141, respectively, with the corresponding predicted amino acid sequences being provided in SEQ ID NO: 142-145, respectively. The DNA and amino acid sequences for these antigens were compared with those in the gene bank as described above. No homologies were found to the 5' end of TbH-29 (which contains the reactive open reading frame), although the 3' end of TbH-29 was
10 found to be identical to the *M. tuberculosis* cosmid Y227. TbH-32 and TbH-33 were found to be identical to the previously identified *M. tuberculosis* insertion element IS6110 and to the *M. tuberculosis* cosmid Y50, respectively. No significant homologies to TbH-30 were found.

Positive phagemid from this additional screening were used to infect *E.*
15 *coli* XL-1 Blue MRF', as described in Sambrook et al., *supra*. Induction of recombinant protein was accomplished by the addition of IPTG. Induced and uninduced lysates were run in duplicate on SDS-PAGE and transferred to nitrocellulose filters. Filters were reacted with human *M. tuberculosis* sera (1:200 dilution) reactive with TbH and a rabbit sera (1:200 or 1:250 dilution) reactive with the N-terminal 4 Kd portion of lacZ.
20 Sera incubations were performed for 2 hours at room temperature. Bound antibody was detected by addition of ¹²⁵I-labeled Protein A and subsequent exposure to film for variable times ranging from 16 hours to 11 days. The results of the immunoblots are summarized in Table 4.

TABLE 4

<u>Antigen</u>	Human M. tb <u>Sera</u>	Anti-lacZ <u>Sera</u>
TbH-29	45 Kd	45 Kd
TbH-30	No reactivity	29 Kd
TbH-32	12 Kd	12 Kd
TbH-33	16 Kd	16 Kd

Positive reaction of the recombinant human *M. tuberculosis* antigens with both the human *M. tuberculosis* sera and anti-lacZ sera indicate that reactivity of the human *M. tuberculosis* sera is directed towards the fusion protein. Antigens reactive with the anti-lacZ sera but not with the human *M. tuberculosis* sera may be the result of the human *M. tuberculosis* sera recognizing conformational epitopes, or the antigen-antibody binding kinetics may be such that the 2 hour sera exposure in the immunoblot is not sufficient.

The results of T-cell assays performed on Tb38-1, ESAT-6 and other representative recombinant antigens are presented in Tables 5A, B and 6, respectively, below:

TABLE 5A
RESULTS OF PBMC PROLIFERATION TO REPRESENTATIVE ANTIGENS

Antigen	Donor										
	1	2	3	4	5	6	7	8	9	10	11
Tb38.1	+++	+	-	-	-	++	-	+	-	++	+++
ESAT-6	+++	+	+	+	-	+	-	+	+	++	+++
TbH-9	++	++	-	++	±	±	++	++	++	++	++

TABLE 5B
RESULTS OF PBMC INTERFERON- γ PRODUCTION TO REPRESENTATIVE ANTIGENS

Antigen	Donor										
	1	2	3	4	5	6	7	8	9	10	11
Tb38.1	+++	+	-	+	+	+++	-	++	-	+++	+++
ESAT-6	+++	+	+	+	+-	+	-	+	+	+++	+++
TbH-9	++	++	-	+++	\pm	\pm	+++	+++	++	+++	++

5

TABLE 6
SUMMARY OF T-CELL RESPONSES TO REPRESENTATIVE ANTIGENS

Antigen	Proliferation			Interferon- γ			total
	patient 4	patient 5	patient 6	patient 4	patient 5	patient 6	
TbH9	++	++	++	+++	++	++	13
TbM7	-	+	-	++	+	-	4
TbH5	-	+	+	++	++	++	8
TbL23	-	+	\pm	++	++	+	7.5
TbH4	-	++	\pm	++	++	\pm	7
- control	-	-	-	-	-	-	0

10 These results indicate that both the inventive *M. tuberculosis* antigens and ESAT-6 can induce proliferation and/or interferon- γ production in T-cells derived from an *M. tuberculosis*-immune individual. To the best of the inventors' knowledge, ESAT-6 has not been previously shown to stimulate human immune responses

15 A set of six overlapping peptides covering the amino acid sequence of the antigen Tb38-1 was constructed using the method described in Example 6. The sequences of these peptides, hereinafter referred to as pep1-6, are provided in SEQ ID Nos. 93-98, respectively. The results of T-cell assays using these peptides are shown in Tables 7 and 8. These results confirm the existence, and help to localize T-cell epitopes within Tb38-1 capable of inducing proliferation and interferon- γ production in T-cells
20 derived from an *M. tuberculosis* immune individual.

TABLE 7
RESULTS OF PBMC PROLIFERATION TO TB38-1 PEPTIDES

[illegible]

TABLE 8
RESULTS OF PBMC INTERFERON- γ PRODUCTION TO TB38-1 PEPTIDES

[illegible]

Studies were undertaken to determine whether the antigens TbH-9 and Tb38-1 represent cellular proteins or are secreted into *M. tuberculosis* culture media. In the first study, rabbit sera were raised against A) secretory proteins of *M. tuberculosis*, B) the known secretory recombinant *M. tuberculosis* antigen 85b, C) recombinant Tb38-1 and D) recombinant TbH-9, using protocols substantially the same as that as described in Example 3A. Total *M. tuberculosis* lysate, concentrated supernatant of *M. tuberculosis* cultures and the recombinant antigens 85b, TbH-9 and Tb38-1 were resolved on denaturing gels, immobilized on nitrocellulose membranes and duplicate blots were probed using the rabbit sera described above.

The results of this analysis using control sera (panel I) and antisera (panel II) against secretory proteins, recombinant 85b, recombinant Tb38-1 and recombinant TbH-9 are shown in Figures 3A-D, respectively, wherein the lane designations are as follows: 1) molecular weight protein standards; 2) 5 μ g of *M. tuberculosis* lysate; 3) 5 μ g secretory proteins; 4) 50 ng recombinant Tb38-1; 5) 50 ng recombinant TbH-9; and 6) 50 ng recombinant 85b. The recombinant antigens were engineered with six terminal histidine residues and would therefore be expected to migrate with a mobility approximately 1 kD larger than the native protein. In Figure 3D, recombinant TbH-9 is lacking approximately 10 kD of the full-length 42 kD antigen, hence the significant difference in the size of the immunoreactive native TbH-9 antigen in the lysate lane (indicated by an arrow). These results demonstrate that Tb38-1 and TbH-9 are intracellular antigens and are not actively secreted by *M. tuberculosis*.

The finding that TbH-9 is an intracellular antigen was confirmed by determining the reactivity of TbH-9-specific human T cell clones to recombinant TbH-9, secretory *M. tuberculosis* proteins and PPD. A TbH-9-specific T cell clone (designated 131TbH-9) was generated from PBMC of a healthy PPD-positive donor. The proliferative response of 131TbH-9 to secretory proteins, recombinant TbH-9 and a control *M. tuberculosis* antigen, TbRa11, was determined by measuring uptake of tritiated thymidine, as described in Example 1. As shown in Figure 4A, the clone 131TbH-9 responds specifically to TbH-9, showing that TbH-9 is not a significant component of *M. tuberculosis* secretory proteins. Figure 4B shows the production of IFN- γ by a second TbH-9-specific T cell clone

(designated PPD 800-10) prepared from PBMC from a healthy PPD-positive donor, following stimulation of the T cell clone with secretory proteins, PPD or recombinant TbH-9. These results further confirm that TbH-9 is not secreted by *M. tuberculosis*.

5 C. USE OF SERA FROM PATIENTS HAVING EXTRAPULMONARY TUBERCULOSIS TO IDENTIFY
DNA SEQUENCES ENCODING *M. TUBERCULOSIS* ANTIGENS

Genomic DNA was isolated from *M. tuberculosis* Erdman strain, randomly sheared and used to construct an expression library employing the Lambda ZAP expression
10 system (Stratagene, La Jolla, CA). The resulting library was screened using pools of sera obtained from individuals with extrapulmonary tuberculosis, as described above in Example 3B, with the secondary antibody being goat anti-human IgG + A + M (H+L) conjugated with alkaline phosphatase.

Eighteen clones were purified. Of these, 4 clones (hereinafter referred to as
15 XP14, XP24, XP31 and XP32) were found to bear some similarity to known sequences. The determined DNA sequences for XP14, XP24 and XP31 are provided in SEQ ID Nos.: 156-158, respectively, with the 5' and 3' DNA sequences for XP32 being provided in SEQ ID Nos.: 159 and 160, respectively. The predicted amino acid sequence for XP14 is provided in SEQ ID No: 161. The reverse complement of XP14 was found to encode the amino acid
20 sequence provided in SEQ ID No.: 162.

Comparison of the sequences for the remaining 14 clones (hereinafter referred to as XP1-XP6, XP17-XP19, XP22, XP25, XP27, XP30 and XP36) with those in the genebank as described above, revealed no homologies with the exception of the 3' ends of XP2 and XP6 which were found to bear some homology to known *M. tuberculosis* cosmids.
25 The DNA sequences for XP27 and XP36 are shown in SEQ ID Nos.: 163 and 164, respectively, with the 5' sequences for XP4, XP5, XP17 and XP30 being shown in SEQ ID Nos: 165-168, respectively, and the 5' and 3' sequences for XP2, XP3, XP6, XP18, XP19, XP22 and XP25 being shown in SEQ ID Nos: 169 and 170; 171 and 172; 173 and 174; 175 and 176; 177 and 178; 179 and 180; and 181 and 182, respectively. XP1 was found to
30 overlap with the DNA sequences for TbH4, disclosed above. The full-length DNA sequence for TbH4-XP1 is provided in SEQ ID No.: 183. This DNA sequence was found to contain an

open reading frame encoding the amino acid sequence shown in SEQ ID No: 184. The reverse complement of TbH4-XP1 was found to contain an open reading frame encoding the amino acid sequence shown in SEQ ID No.: 185. The DNA sequence for XP36 was found to contain two open reading frames encoding the amino acid sequence shown in SEQ ID Nos.: 186 and 187, with the reverse complement containing an open reading frame encoding the amino acid sequence shown in SEQ ID No.: 188.

Recombinant XP1 protein was prepared as described above in Example 3B, with a metal ion affinity chromatography column being employed for purification. As illustrated in Figures 8A-B and 9A-B, using the assays described herein, recombinant XP1 was found to stimulate cell proliferation and IFN- γ production in T cells isolated from an *M. tuberculosis*-immune donors.

D. PREPARATION OF *M. TUBERCULOSIS* SOLUBLE ANTIGENS USING RABBIT ANTI-SERA RAISED AGAINST *M. TUBERCULOSIS* FRACTIONATED PROTEINS

M. tuberculosis lysate was prepared as described above in Example 2. The resulting material was fractionated by HPLC and the fractions screened by Western blot for serological activity with a serum pool from *M. tuberculosis*-infected patients which showed little or no immunoreactivity with other antigens of the present invention. Rabbit anti-sera was generated against the most reactive fraction using the method described in Example 3A. The anti-sera was used to screen an *M. tuberculosis* Erdman strain genomic DNA expression library prepared as described above. Bacteriophage plaques expressing immunoreactive antigens were purified. Phagemid from the plaques was rescued and the nucleotide sequences of the *M. tuberculosis* clones determined.

Ten different clones were purified. Of these, one was found to be TbRa35, described above, and one was found to be the previously identified *M. tuberculosis* antigen, HSP60. Of the remaining eight clones, seven (hereinafter referred to as RDIF2, RDIF5, RDIF8, RDIF10, RDIF11 and RDIF 12) were found to bear some similarity to previously identified *M. tuberculosis* sequences. The determined DNA sequences for RDIF2, RDIF5, RDIF8, RDIF10 and RDIF11 are provided in SEQ ID Nos.: 189-193, respectively, with the corresponding predicted amino acid sequences being provided in SEQ ID Nos: 194-198, respectively. The 5' and 3' DNA sequences for RDIF12 are provided in SEQ ID Nos.: 199

and 200, respectively. No significant homologies were found to the antigen RDIF-7. The determined DNA and predicted amino acid sequences for RDIF7 are provided in SEQ ID Nos.: 201 and 202, respectively. One additional clone, referred to as RDIF6 was isolated, however, this was found to be identical to RDIF5.

Recombinant RDIF6, RDIF8, RDIF10 and RDIF11 were prepared as described above. As shown in Figures 8A-B and 9A-B, these antigens were found to stimulate cell proliferation and IFN- γ production in T cells isolated from *M. tuberculosis*-immune donors.

EXAMPLE 4

PURIFICATION AND CHARACTERIZATION OF A POLYPEPTIDE FROM TUBERCULIN PURIFIED
PROTEIN DERIVATIVE

An *M. tuberculosis* polypeptide was isolated from tuberculin purified protein derivative (PPD) as follows.

PPD was prepared as published with some modification (Seibert, F. et al., Tuberculin purified protein derivative. Preparation and analyses of a large quantity for standard. The American Review of Tuberculosis 44:9-25, 1941).

M. tuberculosis Rv strain was grown for 6 weeks in synthetic medium in roller bottles at 37°C. Bottles containing the bacterial growth were then heated to 100° C in water vapor for 3 hours. Cultures were sterile filtered using a 0.22 µ filter and the liquid phase was concentrated 20 times using a 3 kD cut-off membrane. Proteins were precipitated once with 50% ammonium sulfate solution and eight times with 25% ammonium sulfate solution. The resulting proteins (PPD) were fractionated by reverse phase liquid chromatography (RP-HPLC) using a C18 column (7.8 x 300 mM; Waters, Milford, MA) in a Biocad HPLC system (Perseptive Biosystems, Framingham, MA). Fractions were eluted from the column with a linear gradient from 0-100% buffer (0.1% TFA in acetonitrile). The flow rate was 10 ml/minute and eluent was monitored at 214 nm and 280 nm.

Six fractions were collected, dried, suspended in PBS and tested individually in *M. tuberculosis*-infected guinea pigs for induction of delayed type hypersensitivity (DTH)

reaction. One fraction was found to induce a strong DTH reaction and was subsequently fractionated further by RP-HPLC on a microbore Vydac C18 column (Cat. No. 218TP5115) in a Perkin Elmer/Applied Biosystems Division Model 172 HPLC. Fractions were eluted with a linear gradient from 5-100% buffer (0.05% TFA in acetonitrile) with a flow rate of 80
5 μ l/minute. Eluent was monitored at 215 nm. Eight fractions were collected and tested for induction of DTH in *M. tuberculosis*-infected guinea pigs. One fraction was found to induce strong DTH of about 16 mm induration. The other fractions did not induce detectable DTH. The positive fraction was submitted to SDS-PAGE gel electrophoresis and found to contain a single protein band of approximately 12 kD molecular weight.

10 This polypeptide, herein after referred to as DPPD, was sequenced from the amino terminal using a Perkin Elmer/Applied Biosystems Division Procise 492 protein sequencer as described above and found to have the N-terminal sequence shown in SEQ ID No.: 129. Comparison of this sequence with known sequences in the gene bank as described above revealed no known homologies. Four cyanogen bromide fragments of DPPD were
15 isolated and found to have the sequences shown in SEQ ID Nos.: 130-133.

The ability of the antigen DPPD to stimulate human PBMC to proliferate and to produce IFN- γ was assayed as described in Example 1. As shown in Table 9, DPPD was found to stimulate proliferation and elicit production of large quantities of IFN- γ ; more than that elicited by commercial PPD.

TABLE 9

RESULTS OF PROLIFERATION AND INTERFERON- γ ASSAYS TO DPPD

PBMC Donor	Stimulator	Proliferation (CPM)	IFN- γ (OD ₄₅₀)
A	Medium	1,089	0.17
	PPD (commercial)	8,394	1.29
	DPPD	13,451	2.21
B	Medium	450	0.09
	PPD (commercial)	3,929	1.26
	DPPD	6,184	1.49
C	Medium	541	0.11
	PPD (commercial)	8,907	0.76
	DPPD	23,024	>2.70

5

EXAMPLE 5USE OF REPRESENTATIVE ANTIGENS FOR DIAGNOSIS OF TUBERCULOSIS

This example illustrates the effectiveness of several representative polypeptides in skin tests for the diagnosis of *M. tuberculosis* infection.

Individuals were injected intradermally with 100 μ l of either PBS or PBS plus Tween 20TM containing either 0.1 μ g of protein (for TbH-9 and TbRa35) or 1.0 μ g of protein (for TbRa38-1). Induration was measured between 5-7 days after injection, with a response of 5 mm or greater being considered positive. Of the 20 individuals tested, 2 were PPD negative and 18 were PPD positive. Of the PPD positive individuals, 3 had active tuberculosis, 3 had been previously infected with tuberculosis and 9 were healthy. In a second study, 13 PPD positive individuals were tested with 0.1 μ g TbRa11 in either PBS or PBS plus Tween 20TM as described above. The results of both studies are shown in Table 10.

TABLE 10
RESULTS OF DTH TESTING WITH REPRESENTATIVE ANTIGENS

	TbH-9 Pos/Total	Tb38-1 Pos/Total	TbRa35 Pos/Total	Cumulative Pos/Total	TbRa11 Pos/Total
PPD negative	0/2	0/2	0/2	0/2	
PPD positive					
healthy	5/9	4/9	4/9	6/9	1/4
prior TB	3/5	2/5	2/5	4/5	3/5
active	3/4	3/4	0/4	4/4	1/4
TOTAL	11/18	9/18	6/18	14/18	5/13

5

EXAMPLE 6

SYNTHESIS OF SYNTHETIC POLYPEPTIDES

10 Polypeptides may be synthesized on a Millipore 9050 peptide synthesizer using FMOC chemistry with HPTU (O-Benzotriazole-N,N,N',N'-tetramethyluronium hexafluorophosphate) activation. A Gly-Cys-Gly sequence may be attached to the amino terminus of the peptide to provide a method of conjugation or labeling of the peptide. Cleavage of the peptides from the solid support may be carried out using the following

15 cleavage mixture: trifluoroacetic acid:ethanedithiol:thioanisole:water:phenol (40:1:2:2:3). After cleaving for 2 hours, the peptides may be precipitated in cold methyl-t-butyl-ether. The peptide pellets may then be dissolved in water containing 0.1% trifluoroacetic acid (TFA) and lyophilized prior to purification by C18 reverse phase HPLC. A gradient of 0%-60% acetonitrile (containing 0.1% TFA) in water (containing 0.1% TFA) may be used to elute the

20 peptides. Following lyophilization of the pure fractions, the peptides may be characterized using electrospray mass spectrometry and by amino acid analysis.

EXAMPLE 7PREPARATION AND CHARACTERIZATION OF *M. TUBERCULOSIS* FUSION PROTEINS

5 A fusion protein containing TbRa3, the 38 kD antigen and Tb38-1 was prepared as follows.

Each of the DNA constructs TbRa3, 38 kD and Tb38-1 were modified by PCR in order to facilitate their fusion and the subsequent expression of the fusion protein TbRa3-38 kD-Tb38-1. TbRa3, 38 kD and Tb38-1 DNA was used to perform PCR using the primers PDM-64 and PDM-65 (SEQ ID NO: 146 and 147), PDM-57 and PDM-58 (SEQ ID NO: 148 and 149), and PDM-69 and PDM-60 (SEQ ID NO: 150 and 151), respectively. In each case, the DNA amplification was performed using 10 µl 10X Pfu buffer, 2 µl 10 mM dNTPs, 2 µl each of the PCR primers at 10 µM concentration, 81.5 µl water, 1.5 µl Pfu DNA polymerase (Stratagene, La Jolla, CA) and 1 µl DNA at either 70 ng/µl (for TbRa3) or 50 ng/µl (for 38 kD and Tb38-1). For TbRa3, denaturation at 94°C was performed for 2 min, followed by 40 cycles of 96°C for 15 sec and 72°C for 1 min, and lastly by 72°C for 4 min. For 38 kD, denaturation at 96°C was performed for 2 min, followed by 40 cycles of 96°C for 30 sec, 68°C for 15 sec and 72°C for 3 min, and finally by 72°C for 4 min. For Tb38-1 denaturation at 94°C for 2 min was followed by 10 cycles of 96°C for 15 sec, 68°C for 15 sec and 72°C for 1.5 min, 30 cycles of 96°C for 15 sec, 64°C for 15 sec and 72°C for 1.5, and finally by 72°C for 4 min.

The TbRa3 PCR fragment was digested with NdeI and EcoRI and cloned directly into pT7⁺L2 IL 1 vector using NdeI and EcoRI sites. The 38 kD PCR fragment was digested with Sse8387I, treated with T4 DNA polymerase to make blunt ends and then digested with EcoRI for direct cloning into the pT7⁺L2Ra3-1 vector which was digested with StuI and EcoRI. The 38-1 PCR fragment was digested with Eco47III and EcoRI and directly subcloned into pT7⁺L2Ra3/38kD-17 digested with the same enzymes. The whole fusion was then transferred to pET28b – using NdeI and EcoRI sites. The fusion construct was confirmed by DNA sequencing.

The expression construct was transformed into BLR pLys S *E. coli* (Novagen, Madison, WI) and grown overnight in LB broth with kanamycin (30 µg/ml) and chloramphenicol (34 µg/ml). This culture (12 ml) was used to inoculate 500 ml 2XYT with

the same antibiotics and the culture was induced with IPTG at an OD₅₆₀ of 0.44 to a final concentration of 1.2 mM. Four hours post-induction, the bacteria were harvested and sonicated in 20 mM Tris (8.0), 100 mM NaCl, 0.1% DOC, 20 µg/ml Leupeptin, 20 mM PMSF followed by centrifugation at 26,000 X g. The resulting pellet was resuspended in 8 M urea, 20 mM Tris (8.0), 100 mM NaCl and bound to Pro-bond nickel resin (Invitrogen, Carlsbad, CA). The column was washed several times with the above buffer then eluted with an imidazole gradient (50 mM, 100 mM, 500 mM imidazole was added to 8 M urea, 20 mM Tris (8.0), 100 mM NaCl). The eluates containing the protein of interest were then dialyzed against 10 mM Tris (8.0).

The DNA and amino acid sequences for the resulting fusion protein (hereinafter referred to as TbRa3-38 kD-Tb38-1) are provided in SEQ ID NO: 152 and 153, respectively.

A fusion protein containing the two antigens TbH-9 and Tb38-1 (hereinafter referred to as TbH9-Tb38-1) without a hinge sequence, was prepared using a similar procedure to that described above. The DNA sequence for the TbH9-Tb38-1 fusion protein is provided in SEQ ID NO: 156.

The ability of the fusion protein TbH9-Tb38-1 to induce T cell proliferation and IFN-γ production in PBMC preparations was examined using the protocol described above in Example 1. PBMC from three donors were employed: one who had been previously shown to respond to TbH9 but not Tb38-1 (donor 131); one who had been shown to respond to Tb38-1 but not TbH9 (donor 184); and one who had been shown to respond to both antigens (donor 201). The results of these studies (Figs. 5-7, respectively) demonstrate the functional activity of both the antigens in the fusion protein.

A fusion protein containing TbRa3, the antigen 38kD, Tb38-1 and DPEP was prepared as follows.

Each of the DNA constructs TbRa3, 38 kD and Tb38-1 were modified by PCR and cloned into vectors essentially as described above, with the primers PDM-69 (SEQ ID NO:150 and PDM-83 (SEQ ID NO: 205) being used for amplification of the Tb38-1A fragment. Tb38-1A differs from Tb38-1 by a DraI site at the 3' end of the coding region that

keeps the final amino acid intact while creating a blunt restriction site that is in frame. The TbRa3/38kD/Tb38-1A fusion was then transferred to pET28b using NdeI and EcoRI sites.

DPEP DNA was used to perform PCR using the primers PDM-84 and PDM-85 (SEQ ID NO: 206 and 207, respectively) and 1 µl DNA at 50 ng/µl. Denaturation at 94 °C was performed for 2 min, followed by 10 cycles of 96 °C for 15 sec, 68 °C for 15 sec and 72 °C for 1.5 min; 30 cycles of 96 °C for 15 sec, 64 °C for 15 sec and 72 °C for 1.5 min; and finally by 72 °C for 4 min. The DPEP PCR fragment was digested with EcoRI and Eco72I and clones directly into the pET28Ra3/38kD/38-1A construct which was digested with DraI and EcoRI. The fusion construct was confirmed to be correct by DNA sequencing.

Recombinant protein was prepared as described above. The DNA and amino acid sequences for the resulting fusion protein (hereinafter referred to as TbF-2) are provided in SEQ ID NO: 208 and 209, respectively.

The reactivity of the fusion protein TbF-2 with sera from *M. tuberculosis*-infected patients was examined by ELISA using the protocol described above. The results of these studies (Table 11) demonstrate that all four antigens function independently in the fusion protein.

TABLE 11

REACTIVITY OF TbF-2 FUSION RECOMBINANT WITH TB AND NORMAL SERA

Serum ID	Status	TbF OD450	Status	TbF-2 OD450	Status	ELISA Reactivity			
						38 kD	TbRa3	Tb38-1	DPEP
B931-40	TB	0.57	+	0.321	+	-	+	-	+
B931-41	TB	0.601	+	0.396	+	+	+	+	-
B931-109	TB	0.494	+	0.404	+	+	+	±	-
B931-132	TB	1.502	+	1.292	+	+	+	+	±
5004	TB	1.806	+	1.666	+	±	±	+	-
15004	TB	2.862	+	2.468	+	+	+	+	-
39004	TB	2.443	+	1.722	+	+	+	+	-
68004	TB	2.871	+	2.575	+	+	+	+	-
99004	TB	0.691	+	0.971	+	-	±	+	-
107004	TB	0.875	+	0.732	+	-	±	+	-
92004	TB	1.632	+	1.394	+	+	±	±	-
97004	TB	1.491	+	1.979	+	+	±	-	+
118004	TB	3.182	+	3.045	+	+	±	-	-
173004	TB	3.644	+	3.578	+	+	+	+	-
175004	TB	3.332	+	2.916	+	+	+	-	-
274004	TB	3.696	+	3.716	+	-	+	-	+
276004	TB	3.243	+	2.56	+	-	-	+	-
282004	TB	1.249	+	1.234	+	+	-	-	-
289004	TB	1.373	+	1.17	+	-	+	-	-
308004	TB	3.708	+	3.355	+	-	-	+	-
314004	TB	1.663	+	1.399	+	-	-	+	-
317004	TB	1.163	+	0.92	+	+	-	-	-
312004	TB	1.709	+	1.453	+	-	+	-	-
380004	TB	0.238	-	0.461	+	-	±	-	+
451004	TB	0.18	-	0.2	-	-	-	-	±
478004	TB	0.188	-	0.469	+	-	-	-	±
410004	TB	0.384	+	2.392	+	±	-	-	+
411004	TB	0.306	+	0.874	+	-	+	-	+
421004	TB	0.357	+	1.456	+	-	+	-	+
528004	TB	0.047	-	0.196	-	-	-	-	+
A6-87	Normal	0.094	-	0.063	-	-	-	-	-
A6-88	Normal	0.214	-	0.19	-	-	-	-	-
A6-89	Normal	0.248	-	0.125	-	-	-	-	-
A6-90	Normal	0.179	-	0.206	-	-	-	-	-
A6-91	Normal	0.135	-	0.151	-	-	-	-	-
A6-92	Normal	0.064	-	0.097	-	-	-	-	-
A6-93	Normal	0.072	-	0.098	-	-	-	-	-
A6-94	Normal	0.072	-	0.064	-	-	-	-	-
A6-95	Normal	0.125	-	0.159	-	-	-	-	-
A6-96	Normal	0.121	-	0.12	-	-	-	-	-
Cut-off		0.284		0.266					

One of skill in the art will appreciate that the order of the individual antigens within the fusion protein may be changed and that comparable activity would be expected provided each of the epitopes is still functionally available. In addition, truncated forms of the proteins containing active epitopes may be used in the construction of fusion proteins.

5

From the foregoing, it will be appreciated that, although specific embodiments of the invention have been described herein for the purpose of illustration, various modifications may be made without deviating from the spirit and scope of the invention.

SEQUENCE LISTING

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- (iii) NUMBER OF SEQUENCES: 214
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 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE: 01-OCT-1997
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
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(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 766 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CGAGGCACCG GTAGTTTGAA CCAAACGCAC AATCGACGGG CAAACGAACG GAAGAACACA	60
ACCATGAAGA TGGTGAAATC GATCGCCGCA GGTCTGACCG CCGCGGCTGC AATCGGCGCC	120
GCTGCGGCCG GTGTGACTTC GATCATGGCT GGCGGCCCGG TCGTATACCA GATGCAGCCG	180
GTCGTCTTCG GCGCGCCACT GCCGTTGGAC CCGGCATCCG CCCCTGACGT CCCGACCGCC	240
GCCCAGTTGA CCAGCCTGCT CAACAGCCTC GCCGATCCCA ACGTGTCTGTT TCGGAACAAG	300
GGCAGTCTGG TCGAGGGCGG CATCGGGGGC ACCGAGGCGC GCATCGCCGA CCACAAGCTG	360
AAGAAGGCCG CCGAGCACGG GGATCTGCCG CTGTCTGTTCA GCGTGACGAA CATCCAGCCG	420
GCGGCCGCCG GTTCGGCCAC CGCCGACGTT TCCGTCTCGG GTCCGAAGCT CTCGTGCGCCG	480
GTCACGCAGA ACGTCACGTT CGTGAATCAA GGCGGCTGGA TGCTGTCACG CGCATCGGCG	540
ATGGAGTTGC TGCAGGCCGC AGGGNAACTG ATTGGCGGGC CGGNTTCAGC CCGCTGTTCA	600
GCTACGCCGC CCGCCTGGTG ACGCGTCCAT GTCGAACACT CGCGCGTGTA GCACGGTGCG	660
GTNTGCGCAG GGNCGCACGC ACCGCCCCGT GCAAGCCGTC CTCGAGATAG GTGGTGNCTC	720
GNCACCAGNG ANCACCCCN NNTCGNCNNT TCTCGNTGNT GNATGA	766

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 752 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

ATGCATCACC ATCACCATCA CGATGAAGTC ACGGTAGAGA CGACCTCCGT CTTCCGCGCA	60
GACTTCCTCA GCGAGCTGGA CGCTCCTGCG CAAGCGGGTA CGGAGAGCGC GGTCTCCGGG	120
GTGGAAGGGC TCCCGCCGGG CTCGGCGTTG CTGGTAGTCA AACGAGGCC CAACGCCGGG	180
TCCCGGTTCC TACTCGACCA AGCCATCACG TCGGCTGGTC GGCATCCCGA CAGCGACATA	240
TTTCTCGACG ACGTGACCGT GAGCCGTGCG CATGCTGAAT TCCGGTTGGA AAACAACGAA	300
TTCAATGTCG TCGATGTCGG GAGTCTCAAC GGCACCTACG TCAACCGCGA GCCCGTGGAT	360
TCGGCGGTGC TGGCGAACGG CGACGAGGTC CAGATCGGCA AGCTCCGGTT GGTGTTCTTG	420
ACCGGACCCA AGCAAGGCGA GGATGACGGG AGTACCGGGG GCCCGTGAGC GCACCCGATA	480
GCCCCGCGCT GGCCGGGATG TCGATCGGGG CGGTCCTCCG ACCTGCTACG ACCGGATTTT	540
CCCTGATGTC CACCATCTCC AAGATTCGAT TCTTGGGAGG CTTGAGGGTC NGGGTGACCC	600
CCCCGCGGGC CTCATTTCNGG GGTNTCGGCN GGTTTCACCC CNTACCNACT GCCNCCCGGN	660

TTGCNAATTC NTTCTTCNCT GCCCNNAAG GGACCNTTAN CTTGCCGCTN GAAANGGTNA 720
 TCCNNGGGCCC NTCCTNGAAN CCCCNTCCCC CT 752

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 813 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CATATGCATC ACCATCACCA TCACACTTCT AACCGCCCAG CGCGTCGGGG GCGTCGAGCA 60
 CCACGCGACA CCGGGCCCGA TCGATCTGCT AGCTTGAGTC TGGTCAGGCA TCGTCGTCAG 120
 CAGCGCGATG CCCTATGTTT GTCGTCGACT CAGATATCGC GGCAATCCAA TCTCCCGCCT 180
 GCGGCCGGCG GTGCTGCAAA CTACTCCCGG AGGAATTTTCG ACGTGCGCAT CAAGATCTTC 240
 ATGCTGGTCA CGGCTGTCGT TTTGCTCTGT TGTTCGGGTG TGGCCACGGC CGCGCCCAAG 300
 ACCTACTGCG AGGAGTTGAA AGGCACCGAT ACCGGCCAGG CGTGCCAGAT TCAAATGTCC 360
 GACCCGGCCT ACAACATCAA CATCAGCCTG CCCAGTTACT ACCCGACCA GAAGTCGCTG 420
 GAAAATTACA TCGCCAGAC GCGCGACAAG TTCCTCAGCG CGGCCACATC GTCCACTCCA 480
 CGCGAAGCCC CCTACGAATT GAATATCACC TCGGCCACAT ACCAGTCCGC GATACCGCCG 540
 CGTGGTACGC AGGCCGTGGT GCTCAMGGTC TACCACAACG CCGGCGGCAC GCACCCAACG 600
 ACCACGTACA AGGCCTTCGA TTGGGACCAG GCCTATCGCA AGCCAATCAC CTATGACACG 660
 CTGTGGCAGG CTGACACCGA TCCGCTGCCA GTCGTCTTCC CCATTGTTGC AAGGTGAACT 720
 GAGCAACGCA GACCGGGACA ACWGGTATCG ATAGCCGCCN AATGCCGGCT TGAACCCNG 780
 TGAAATTATC ACAACTTCGC AGTCACNAAA NAA 813

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 447 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CGGTATGAAC ACGGCCGCGT CCGATAACTT CCAGCTGTCC CAGGGTGGGC AGGGATTTCG 60

CATTCCGATC GGGCAGGCGA TGGCGATCGC GGGCCAGATC CGATCGGGTG GGGGGTCACC	120
CACCGTTCAT ATCGGGCCTA CCGCCTTCCT CGGCTTGGGT GTTGTCGACA ACAACGGCAA	180
CGGCGCACGA GTCCAACGCG TGGTCGGGAG CGCTCCGGCG GCAAGTCTCG GCATCTCCAC	240
CGGCGACGTG ATCACCGCGG TCGACGGCGC TCCGATCAAC TCGGCCACCG CGATGGCGGA	300
CGCGCTTAAC GGGCATCATC CCGGTGACGT CATCTCGGTG AACTGGCAAA CCAAGTCGGG	360
CGGCACGCGT ACAGGGAACG TGACATTGGC CGAGGGACCC CCGGCCTGAT TTCGTCGYGG	420
ATACCACCCG CCGGCCGGCC AATTGGA	447

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 604 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GTCCCACTGC GGTCGCCGAG TATGTCGCCC AGCAAATGTC TGGCAGCCGC CCAACGGAAT	60
CCGGTGATCC GACGTGCGAG GTTGTCGAAC CCGCCGCCGC GGAAGTATCG GTCCATGCCT	120
AGCCCGGCGA CGGCGAGCGC CGGAATGGCG CGAGTGAGGA GGCGGGCAAT TTGGCGGGGC	180
CCGGCGACGG NGAGCGCCGG AATGGCGCGA GTGAGGAGGT GGNCAGTCAT GCCCAGNGTG	240
ATCCAATCAA CCTGNATTCG GNCTGNNGGN CCATTTGACA ATCGAGGTAG TGAGCGCAAA	300
TGAATGATGG AAAACGGGNG GNGACGTCCG NTGTTCTGGT GGTGNTAGGT GNCTGNCTGG	360
NGTNGNGGNT ATCAGGATGT TCTTCGNCGA AANCTGATGN CGAGGAACAG GGTGTNCCCG	420
NNANNCCNAN GGNGTCCNAN CCCNNNNTCC TCGNCGANAT CANANAGNCG NTTGATGNGA	480
NAAAAGGGTG GANCAGNNNN AANTNGNGGN CCNAANAANC NNNANNGNNG NNAGNTNGNT	540
NNNTNTTNNC ANNNNNNTG NNGNNGNNCN NNNCAANCNN NTNNNNGNAA NNGGNTTNTT	600
NAAT	604

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 633 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TTGCANGTCG AACCACCTCA CTAAAGGGAA CAAAAGCTNG AGCTCCACCG CGGTGGCGGC	60
CGCTCTAGAA CTAGTGKATM YYYCKGGCTG CAGSAATYCG GYACGAGCAT TAGGACAGTC	120
TAACGGTCCT GTTACGGTGA TCGAATGACC GACGACATCC TGCTGATCGA CACCGACGAA	180
CGGGTGCGAA CCCTCACCT CAACCGGCCG CAGTCCCGYA ACGCGCTCTC GGCGGCGCTA	240
CGGGATCGGT TTTTCGCGGY GTTGGYCGAC GCCGAGGYCG ACGACGACAT CGACGTCGTC	300
ATCCTCACCG GYGCCGATCC GGTGTTCTGC GCCGGACTGG ACCTCAAGGT AGCTGGCCGG	360
GCAGACCGCG CTGCCGGACA TCTCACCGCG GTGGGCGGCC ATGACCAAGC CGGTGATCGG	420
CGCGATCAAC GGCGCCGCGG TCACCGGCGG GCTCGAACTG GCGCTGTACT GCGACATCCT	480
GATCGCCTCC GAGCACGCCC GCTTCGNCGA CACCCACGCC CGGGTGGGGC TGCTGCCCAC	540
CTGGGGACTC AGTGTGTGCT TGCCGAAAA GGTGCGCATC GGNCTGGGCC GGTGGATGAG	600
CCTGACCGGC GACTACCTGT CCGTGACCGA CGC	633

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1362 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CGACGACGAC GGCGCCGGAG AGCGGGCGCG AACGGCGATC GACGCGGCC TGGCCAGAGT	60
CGGCACCACC CAGGAGGGAG TCGAATCATG AAATTTGTCA ACCATATTGA GCCCGTCGCG	120
CCCCGCCGAG CCGGCGGCGC GGTCGCCGAG GTCTATGCCG AGGCCCGCCG CGAGTTCGGC	180
CGGCTGCCCC AGCCGCTCGC CATGCTGTCC CCGGACGAGG GACTGCTCAC CGCCGGCTGG	240
GCGACGTTGC GCGAGAACT GCTGGTGGGC CAGGTGCCGC GTGGCCGCAA GGAAGCCGTC	300
GCCGCCGCCG TCGCGGCCAG CCTGCGCTGC CCCTGGTGCG TCGACGACA CACCACCATG	360
CTGTACGCGG CAGGCCAAAC CGACACCGCC GCGGCGATCT TGGCCGGCAC AGCACCTGCC	420
GCCGGTGACC CGAACGCGCC GTATGTGGCG TGGGCGGCAG GAACCGGGAC ACCGGCGGGA	480
CCGCCGGCAC CGTTCGGCCC GGATGTCGCC GCCGAATACC TGGGCACCGC GGTGCAATTC	540
CACTTCATCG CACGCCTGGT CCTGGTGTGCT CTGGACGAAA CCTTCCTGCC GGGGGGCCCCG	600
CGCGCCCAAC AGCTCATGCG CCGCGCCGGT GGACTGGTGT TCGCCCGCAA GGTGCGCGCG	660
GAGCATCGGC CGGGCCGCTC CACCCGCCG CTCGAGCCGC GAACGCTGCC CGACGATCTG	720

GCATGGGCAA CACCGTCCGA GCCCATAGCA ACCGCGTTTCG CCGCGCTCAG CCACCACCTG	780
GACACCGCGC CGCACCTGCC GCCACCGACT CGTCAGGTGG TCAGGCGGGT CGTGGGGTTCG	840
TGGCACGGCG AGCCAATGCC GATGAGCAGT CGCTGGACGA ACGAGCACAC CGCCGAGCTG	900
CCCGCCGACC TGCACGCGCC CACCCGTCTT GCCCTGCTGA CCGGCCTGGC CCCGCATCAG	960
GTGACCGACG ACGACGTCGC CGCGGGCCGA TCCCTGCTCG ACACCGATGC GGCGCTGGTT	1020
GGCGCCCTGG CCTGGGCGCG CTTACCGCC GCGCGGCGCA TCGGCACCTG GATCGGCGCC	1080
GCCGCCGAGG GCCAGGTGTC GCGGCAAAAC CCGACTGGGT GAGTGTGCGC GCCCTGTCGG	1140
TAGGGTGTCA TCGCTGGCCC GAGGGATCTC GCGGCGGCGA ACGGAGGTGG CGACACAGGT	1200
GGAAGCTGCG CCCACTGGCT TGCGCCCCAA CGCCGTCGTG GGCGTTCGGT TGGCCGCACT	1260
GGCCGATCAG GTCGGCGCCG GCCCTTGCC GAAGGTCCAG CTCAACGTGC CGTCACCGAA	1320
GGACCGGACG GTCACCGGGG GTCACCCTGC GCGCCCAAGG AA	1362

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1458 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GCGACGACCC CGATATGCCG GGCACCGTAG CGAAAGCCGT CGCCGACGCA CTCGGGCGCG	60
GTATCGCTCC CGTTGAGGAC ATTCAGGACT GCGTGGAGGC CCGGCTGGGG GAAGCCGGTC	120
TGGATGACGT GGCCCGTGTT TACATCATCT ACCGGCAGCG GCGCGCCGAG CTGCGGACGG	180
CTAAGGCCTT GCTCGGCGTG CGGGACGAGT TAAAGCTGAG CTTGGCGGCC GTGACGGTAC	240
TGCGCGAGCG CTATCTGCTG CACGACGAGC AGGGCCGGCC GGCCGAGTCG ACCGGCGAGC	300
TGATGGACCG ATCGGCGCGC TGTGTCGCG CGGCCGAGGA CCAGTATGAG CCGGGCTCGT	360
CGAGGCGGTG GGCCGAGCGG TTCGCCACGC TATTACGCAA CCTGGAATTC CTGCCGAATT	420
CGCCCACGTT GATGAACTCT GGCACCGACC TGGGACTGCT CGCCGGCTGT TTTGTTCTGC	480
CGATTGAGGA TTCGCTGCAA TCGATCTTTG CGACGCTGGG ACAGGCCGCC GAGCTGCAGC	540
GGGCTGGAGG CGGCACCGGA TATGCGTTCA GCCACCTGCG ACCCGCCGGG GATCGGGTGG	600
CCTCCACGGG CGGCACGGCC AGCGGACCGG TGTCGTTTCT ACGGCTGTAT GACAGTGCCG	660
CGGGTGTGGT CTCCATGGGC GGTGCGCCGC GTGGCGCCTG TATGGCTGTG CTTGATGTGT	720
CGCACCCGGA TATCTGTGAT TTCGTACCG CCAAGGCCGA ATCCCCAGC GAGCTCCCGC	780

ATTTCAACCT ATCGGTTGGT GTGACCGACG CGTTCCTGCG GGCCGTCGAA CGCAACGGCC	840
TACACCGGCT GGTCAATCCG CGAACCGGCA AGATCGTCGC GCGGATGCCC GCCGCCGAGC	900
TGTTTCGACGC CATCTGCAAA GCCGCGCACG CCGGTGGCGA TCCCAGGCTG GTGTTTCTCG	960
ACACGATCAA TAGGGCAAAC CCGGTGCCGG GGAGAGGCCG CATCGAGGCG ACCAACCCGT	1020
GCGGGGAGGT CCCACTGCTG CTTACGAGT CATGTAATCT CGGCTCGATC AACCTCGCCC	1080
GGATGCTCGC CGACGGTCGC GTCGACTGGG ACCGGCTCGA GGAGGTCGCC GGTGTGGCGG	1140
TGCGGTTTCCT TGATGACGTC ATCGATGTCA GCCGCTACCC CTTCCCCGAA CTGGGTGAGG	1200
CGGCCCCGCGC CACCCGCAAG ATCGGGCTGG GAGTCATGGG TTTGGCGGAA CTGCTTGCCG	1260
CACTGGGTAT TCCGTACGAC AGTGAAGAAG CCGTGCGGTT AGCCACCCGG CTCATGCGTC	1320
GCATACAGCA GGCGGCGCAC ACGGCATCGC GGAGGCTGGC CGAAGAGCGG GGCGCATTCC	1380
CGGCGTTTAC CGATAGCCGG TTCGCGCGGT CGGGCCCGAG GCGCAACGCA CAGGTCACCT	1440
CCGTCGCTCC GACGGGCA	1458

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 862 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ACGGTGTAAT CGTGCTGGAT CTGGAACCGC GTGGCCCGCT ACCTACCGAG ATCTACTGGC	60
GGCGCAGGGG GCTGGCCCTG GGCATCGCGG TCGTCGTAGT CGGGATCGCG GTGGCCATCG	120
TCATCGCCTT CGTCGACAGC AGCGCCGGTG CCAAACCGGT CAGCGCCGAC AAGCCGGCCT	180
CCGCCCAGAG CCATCCGGGC TCGCCGGCAC CCCAAGCACC CCAGCCGGCC GGGCAAACCG	240
AAGGTAACGC CGCCGCGGCC CCGCCGCAGG GCCAAAACCC CGAGACACCC ACGCCCACCG	300
CCGCGGTGCA GCCGCGCCG GTGCTCAAGG AAGGGGACGA TTGCCCCGAT TCGACGCTGG	360
CCGTCAAAGG TTTGACCAAC GCGCCGCAGT ACTACGTCGG CGACCAGCCG AAGTTCACCA	420
TGGTGGTCAC CAACATCGGC CTGGTGTCTT GTAAACGCGA CGTTGGGGCC GCGGTGTTGG	480
CCGCCTACGT TTA CTGCTG GACAACAAGC GGTGTGTGGT CAACCTGGAC TCGCGGCCCT	540
CGAATGAGAC GCTGGTCAAG ACGTTTTCCC CCGGTGAGCA GGTAACGACC GCGGTGACCT	600
GGACCGGGAT GGGATCGGCG CCGCGCTGCC CATTGCCGCG GCCGGCGATC GGGCCGGGCA	660
CCTACAATCT CGTGGTACAA CTGGGCAATC TCGGCTCGCT GCCGGTTCCG TTCATCCTGA	720

ATCAGCCGCC GCGCCGCCC GGGCCGGTAC CCGCTCCGGG TCCAGCGCAG GCGCCTCCGC	780
CGGAGTCTCC CGCGCAAGGC GGATAATTAT TGATCGCTGA TGGTCGATTC CGCCAGCTGT	840
GACAACCCCT CGCCTCGTGC CG	862

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 622 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TTGATCAGCA CCGGCAAGGC GTCACATGCC TCCCTGGGTG TGCAGGTGAC CAATGACAAA	60
GACACCCCGG GCGCCAAGAT CGTCGAAGTA GTGGCCGGTG GTGCTGCCGC GAACGCTGGA	120
GTGCCGAAGG GCGTCGTTGT CACCAAGGTC GACGACCGCC CGATCAACAG CGCGGACGCG	180
TTGGTTGCCG CCGTGCGGTC CAAAGCGCCG GCGCCACGG TGGCGCTAAC CTTTCAGGAT	240
CCCTCGGGCG GTAGCCGCAC AGTGCAAGTC ACCCTCGGCA AGGCGGAGCA GTGATGAAGG	300
TCGCCGCGCA GTGTTCAAAG CTCGGATATA CCGTGGCACC CATGGAACAG CGTGCGGAGT	360
TGGTGGTTGG CCGGGCACTT GTCGTCGTCG TTGACGATCG CACGGCGCAC GGCGATGAAG	420
ACCACAGCGG GCCGCTTGTC ACCGAGCTGC TCACCGAGGC CGGGTTTGTT GTCGACGGCG	480
TGGTGGCGGT GTCGGCCGAC GAGGTCGAGA TCCGAAATGC GCTGAACACA GCGGTGATCG	540
GCGGGGTGGA CCTGGTGGTG TCGGTCGGCG GGACCGGNGT GACGNCTCGC GATGTCACCC	600
CGGAAGCCAC CCGNGACATT CT	622

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1200 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GGCGCAGCGG TAAGCCTGTT GGCCGCCGGC ACCTGGTGT TGACAGCATG CGGCGGTGGC	60
ACCAACAGCT CGTCGTCAGG CGCAGGCGGA ACGTCTGGGT CGGTGCACTG CGGCGGCAAG	120
AAGGAGCTCC ACTCCAGCGG CTCGACCGCA CAAGAAAATG CCATGGAGCA GTTCGTCTAT	180

GCCTACGTGC GATCGTGCCC GGGCTACACG TTGGACTACA ACGCCAACGG GTCCGGTGCC	240
GGGGTGACCC AGTTTCTCAA CAACGAAACC GATTTTCGCC GCTCGGATGT CCCGTTGAAT	300
CCGTCGACCG GTCAACCTGA CCGGTCGGCG GAGCGGTGCG GTTCCCCGGC ATGGGACCTG	360
CCGACGGTGT TCGGCCCCGAT CGCGATCACC TACAATATCA AGGGCGTGAG CACGCTGAAT	420
CTTGACGGAC CCACTACCGC CAAGATTTTC AACGGCACCA TCACCGTGTG GAATGATCCA	480
CAGATCCAAG CCCTCAACTC CGGCACCGAC CTGCCGCCAA CACCGATTAG CGTTATCTTC	540
CGCAGCGACA AGTCCGGTAC GTCGGACAAC TTCCAGAAAT ACCTCGACGG TGTATCCAAC	600
GGGGCGTGGG GCAAAGGCGC CAGCGAAACG TTCAGCGGGG GCGTCGGCGT CGGCGCCAGC	660
GGGAACAACG GAACGTCGGC CCTACTGCAG ACGACCGACG GGTCGATCAC CTACAACGAG	720
TGGTCGTTTG CGGTGGGTAA GCAGTTGAAC ATGGCCAGA TCATCACGTC GGCGGGTCCG	780
GATCCAGTGG CGATCACCAC CGAGTCGGTC GGTAAGACAA TCGCCGGGGC CAAGATCATG	840
GGACAAGGCA ACGACCTGGT ATTGGACACG TCGTCGTTCT ACAGACCCAC CCAGCCTGGC	900
TCTTACCCGA TCGTGCTGGC GACCTATGAG ATCGTCTGCT CGAAATACCC GGATGCGACG	960
ACCGGTACTG CGGTAAGGGC GTTTATGCAA GCCGCGATTG GTCCAGGCCA AGAAGGCCTG	1020
GACCAATACG GCTCCATTCC GTTGCCCAA TCGTTCCAAG CAAAATTGGC GGCCGCGGTG	1080
AATGCTATTT CTTGACCTAG TGAAGGGAAT TCGACGGTGA GCGATGCCGT TCCGCAGGTA	1140
GGGTCGCAAT TTGGGCCGTA TCAGCTATTG CGGCTGCTGG GCCGAGGCGG GATGGGCGAG	1200

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1155 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GCAAGCAGCT GCAGGTCGTG CTGTTTCGACG AACTGGGCAT GCCGAAGACC AAACGCACCA	60
AGACCGGCTA CACCACGGAT GCCGACGCGC TGCAGTCGTT GTTCGACAAG ACCGGGCATC	120
CGTTTCTGCA ACATCTGCTC GCCCACC GCG ACGTCACCCG GCTCAAGGTC ACCGTCGACG	180
GGTTGCTCCA AGCGGTGGCC GCCGACGGCC GCATCCACAC CACGTTCAAC CAGACGATCG	240
CCGCGACCGG CCGGCTCTCC TCGACCGAAC CCAACCTGCA GAACATCCCG ATCCGCACCG	300
ACGCGGGCCG GCGGATCCGG GACGCGTTTCG TGGTCGGGGA CGGTTACGCC GAGTTGATGA	360
CGGCCGACTA CAGCCAGATC GAGATGCGGA TCATGGGGCA CCTGTCCGGG GACGAGGGCC	420

TCATCGAGGC GTTCAACACC GGGGAGGACC TGTATTCGTT CGTCGCGTCC CGGGTGTTCG	480
GTGTGCCCCAT CGACGAGGTC ACCGGCGAGT TCGGGCGCCG GGTCAAGGCG ATGTCCTACG	540
GGCTGGTTTA CGGGTTGAGC GCCTACGGCC TGTCGCAGCA GTTGAAAATC TCCACCGAGG	600
AAGCCAACGA GCAGATGGAC GCGTATTTTCG CCCGATTCGG CGGGGTGCGC GACTACCTGC	660
GCGCCGTAGT CGAGCGGGCC CGCAAGGACG GCTACACCTC GACGGTGCTG GGCCGTGCGC	720
GCTACCTGCC CGAGCTGGAC AGCAGCAACC GTCAAGTGCG GGAGGCCGCC GAGCGGGCGG	780
CGCTGAACGC GCCGATCCAG GGCAGCGCGG CCGACATCAT CAAGGTGGCC ATGATCCAGG	840
TCGACAAGGC GCTCAACGAG GCACAGCTGG CGTCGCGCAT GCTGCTGCAG GTCCACGACG	900
AGCTGCTGTT CGAAATCGCC CCCGGTGAAC GCGAGCGGGT CGAGGCCCTG GTGCGCGACA	960
AGATGGGCGG CGCTTACCCG CTCGACGTCC CGCTGGAGGT GTCGGTGGGC TACGGCCGCA	1020
GCTGGGACGC GGC GGCGCAC TGAGTGCCGA GCGTGTCATCT GGGGCGGGAA TTCGGCGATT	1080
TTTCCGCCCT GAGTTCACGC TCGGCGCAAT CGGGACCGAG TTTGTCCAGC GTGTACCCGT	1140
CGAGTAGCCT CGTCA	1155

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1771 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GAGCGCCGTC TGGTGTTTGA ACGGTTTTAC CGGTCGGCAT CGGCACGGGC GTTGCCGGGT	60
TCGGGCCTCG GGTGGCGAT CGTCAAACAG GTGGTGCTCA ACCACGGCGG ATTGCTGCGC	120
ATCGAAGACA CCGACCCAGG CGGCCAGCCC CCTGGAACGT CGATTTACGT GCTGCTCCCC	180
GGCCGTGCGA TGCCGATTCC GCAGCTTCCC GGTGCGACGG CTGGCGCTCG GAGCACGGAC	240
ATCGAGAACT CTCGGGGTTC GGCGAACGTT ATCTCAGTGG AATCTCAGTC CACGCGCGCA	300
ACCTAGTTGT GCAGTTACTG TTGAAAGCCA CACCCATGCC AGTCCACGCA TGGCCAAGTT	360
GGCCCGAGTA GTGGGCCTAG TACAGGAAGA GCAACCTAGC GACATGACGA ATCACCACG	420
GTATTCGCCA CCGCCGAGC AGCCGGGAAC CCCAGGTTAT GCTCAGGGGC AGCAGCAAAC	480
GTACAGCCAG CAGTTCGACT GGC GTTACCC ACCGTCCCCG CCCCCGCAGC CAACCCAGTA	540
CCGTCAACCC TACGAGGCGT TGGGTGGTAC CCGGCCGGGT CTGATACCTG GCGTGATTCC	600
GACCATGACG CCCCCTCCTG GGATGGTTTCG CCAACGCCCT CGTGCAGGCA TGTTGGCCAT	660

CGGCGCGGTG ACGATAGCGG TGGTGTCCGC CGGCATCGGC GGCGCGGCCG CATCCCTGGT	720
CGGGTTCAAC CGGGCACCCG CCGGCCCCAG CGGCGGCCCA GTGGCTGCCA GCGCGGCGCC	780
AAGCATCCCC GCAGCAAACA TGCCGCCGGG GTCGGTCGAA CAGGTGGCGG CCAAGGTGGT	840
GCCCAGTGTC GTCATGTTGG AAACCGATCT GGGCCGCCAG TCGGAGGAGG GCTCCGGCAT	900
CATTCTGTCT GCCGAGGGGC TGATCTTGAC CAACAACCAC GTGATCGCGG CGGCCGCCAA	960
GCCTCCCCTG GGCAGTCCGC CGCCGAAAAC GACGGTAACC TTCTCTGACG GGCGGACCGC	1020
ACCCTTCACG GTGGTGGGGG CTGACCCAC CAGTGATATC GCCGTCGTCC GTGTTCAAGG	1080
CGTCTCCGGG CTCACCCCGA TCTCCCTGGG TTCCTCCTCG GACCTGAGGG TCGGTCAGCC	1140
GGTGCTGGCG ATCGGGTCGC CGCTCGGTTT GGAGGGCACC GTGACCACGG GGATCGTCAG	1200
CGCTCTCAAC CGTCCAGTGT CGACGACCGG CGAGGCCGGC AACCAGAACA CCGTGCTGGA	1260
CGCCATTAG ACCGACGCCG CGATCAACCC CGGTAACCTC GGGGGCGCGC TGGTGAACAT	1320
GAACGCTCAA CTCGTCGGAG TCAACTCGGC CATTGCCACG CTGGGCGCGG ACTCAGCCGA	1380
TGCGCAGAGC GGCTCGATCG GTCTCGGTTT TGCGATTCCA GTCGACCAGG CCAAGCGCAT	1440
CGCCGACGAG TTGATCAGCA CCGGCAAGGC GTCACATGCC TCCCTGGGTG TGCAGGTGAC	1500
CAATGACAAA GACACCCCGG GCGCCAAGAT CGTCGAAGTA GTGGCCGGTG GTGCTGCCGC	1560
GAACGCTGGA GTGCCGAAGG GCGTCGTTGT CACCAAGGTC GACGACCGCC CGATCAACAG	1620
CGCGGACGCG TTGGTTGCCG CCGTGCGGTC CAAAGCGCCG GGCGCCACGG TGGCGCTAAC	1680
CTTTCAGGAT CCCTCGGGCG GTAGCCGCAC AGTGCAAGTC ACCCTCGGCA AGGCGGAGCA	1740
GTGATGAAGG TCGCCGCGCA GTGTTCAAAG C	1771

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1058 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CTCCACCGCG GTGGCGGCCG CTCTAGAACT AGTGGATCCC CCGGGCTGCA GGAATTCGGC	60
ACGAGGATCC GACGTCGAG GTTGTGGAAC CCGCCGCCGC GGAAGTATCG GTCCATGCCT	120
AGCCCGGCGA CGGCGAGCGC CGGAATGGCG CGAGTGAGGA GGCGGGCAAT TTGGCGGGGC	180
CCGGCGACGG CGAGCGCCG AATGGCGCGA GTGAGGAGGC GGGCAGTCAT GCCAGCGTG	240
ATCCAATCAA CCTGCATTCG GCCTGCGGGC CCATTTGACA ATCGAGGTAG TGAGCGCAAA	300

TGAATGATGG AAAACGGGCG GTGACGTCCG CTGTTCTGGT GGTGCTAGGT GCCTGCCTGG	360
CGTTGTGGCT ATCAGGATGT TCTTCGCCGA AACCTGATGC CGAGGAACAG GGTGTTCCCG	420
TGAGCCCCGAC GGCCTCCGAC CCCGCGCTCC TCGCCGAGAT CAGGCAGTCG CTTGATGCGA	480
CAAAAGGGTT GACCAGCGTG CACGTAGCGG TCCGAACAAC CGGGAAAGTC GACAGCTTGC	540
TGGGTATTAC CAGTGCCGAT GTCGACGTCC GGGCCAATCC GCTCGCGGCA AAGGGCGTAT	600
GCACCTACAA CGACGAGCAG GGTGTCCCGT TTCGGGTACA AGGCGACAAC ATCTCGGTGA	660
AACTGTTCTGA CGACTGGAGC AATCTCGGCT CGATTTCTGA ACTGTCAACT TCACGCGTGC	720
TCGATCCTGC CGCTGGGGTG ACGCAGCTGC TGTCCGGTGT CACGAACCTC CAAGCGCAAG	780
GTACCGAAGT GATAGACGGA ATTTGACCA CAAAATCAC CGGGACCATC CCCGCGAGCT	840
CTGTCAAGAT GCTTGATCCT GCGGCCAAGA GTGCAAGGCC GCGGACCGTG TGGATTGCCC	900
AGGACGGCTC GCACCACCTC GTCCGAGCGA GCATCGACCT CGGATCCGGG TCGATTCAGC	960
TCACGCAGTC GAAATGGAAC GAACCCGTCA ACGTCGACTA GGCCGAAGTT GCGTCGACGC	1020
GTTGNTCGAA ACGCCCTTGT GAACGGTGTC AACGGNAC	1058

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 542 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GAATTCGGCA CGAGAGGTGA TCGACATCAT CGGGACCAGC CCCACATCCT GGGAACAGGC	60
GGCGGCGGAG GCGGTCCAGC GGGCGCGGGA TAGCGTCGAT GACATCCGCG TCGCTCGGGT	120
CATTGAGCAG GACATGGCCG TGGACAGCGC CGGCAAGATC ACCTACCGCA TCAAGCTCGA	180
AGTGTCGTTT AAGATGAGGC CGGCGCAACC GCGCTAGCAC GGGCCGGCGA GCAAGACGCA	240
AAATCGCACG GTTTGCGGTT GATTCGTGCG ATTTTGTGTC TGCTCGCCGA GGCCTACCAG	300
GCGCGGCCCA GGTCCGCGTG CTGCCGTATC CAGGCGTGCA TCGCGATTCC GCGGCCCACG	360
CCGAGATTAA TGCTTCGCGT CGACCCGAAC TGGGCGATCC GCCGGNGAGC TGATCGATGA	420
CCGTGGCCAG CCCGTCGATG CCCGAGTTGC CCGAGGAAAC GTGCTGCCAG GCCGGTAGGA	480
AGCGTCCGTA GGCGGCGGTG CTGACCGGCT CTGCCTGCGC CCTCAGTGCG GCCAGCGAGC	540
GG	542

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 913 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CGGTGCCGCC CGCGCCTCCG TTGCCCCCAT TGCCGCCGTC GCCGATCAGC TGCGCATCGC	60
CACCATCACC GCCTTTGCCG CCGGCACCGC CGGTGGCGCC GGGGCCGCCG ATGCCACCGC	120
TTGACCTTGG CCGCCGGCGC CGCCATTGCC ATACAGCACC CCGCCGGGGG CACCGTTACC	180
GCCGTCGCCA CCGTCGCCGC CGCTGCCGTT TCAGGCCGGG GAGGCCGAAT GAACCGCCGC	240
CAAGCCCGCC GCCGGCACCG TTGCCGCCTT TTCCGCCCGC CCCGCCGGCG CCGCCAATTG	300
CCGAACAGCC AMGCACCGTT GCCGCCAGCC CCGCCGCCGT TAACGGCGCT GCCGGGCGCC	360
GCCGCCGGAC CCGCCATTAC CGCCGTTCCC GTTCGGTGCC CCGCCGTTAC CGGCGCCGCC	420
GTTTGCCGCC AATATTCGGC GGGCACCGCC AGACCCGCCG GGGCCACCAT TGCCGCCGGG	480
CACCGAAACA ACAGCCCAAC GGTGCCGCCG GCCCCGCCGT TTGCCGCCAT CACCGGCCAT	540
TCACCGCCAG CACCGCCGTT AATGTTTATG AACCCGGTAC CGCCAGCGCG GCCCCTATTG	600
CCGGGCGCCG GAGNGCGTGC CCGCCGGCGC CGCCAACGCC CAAAAGCCCG GGGTTGCCAC	660
CGGCCCCGCC GGACCCACCG GTCCCGCCGA TCCCCCGTT GCCGCCGGTG CCGCCGCCAT	720
TGGTGCTGCT GAAGCCGTTA GCGCCGGTTC CGCSGGTTCC GGCGGTGGCG CCNTGGCCGC	780
CGGCCCCGCC GTTGCCGTAC AGCCACCCCC CGGTGGCGCC GTTGCCGCCA TTGCCGCCAT	840
TGCCGCCGTT GCCGCCATTG CCGCCGTTCC CGCCGCCACC GCCGNTTG CCGCCGGCGC	900
CGCCGGCGGC CGC	913

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1872 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GACTACGTTG GTGTAGAAAA ATCCTGCCGC CCGGACCCTT AAGGCTGGGA CAATTTCTGA	60
TAGCTACCCC GACACAGGAG GTTACGGGAT GAGCAATTCG CGCCGCCGCT CACTCAGGTG	120

GTCATGGTTG CTGAGCGTGC TGGCTGCCGT CGGGCTGGGC CTGGCCACGG CGCCGGCCCA	180
GGCGGCCCCG CCGGCCTTGT CGCAGGACCG GTTCGCCGAC TTCCCCGCGC TCCCCCTCGA	240
CCCGTCCGCG ATGGTTCGCCC AAGTGGCGCC ACAGGTGGTC AACATCAACA CCAAACCTGGG	300
CTACAACAAC GCCGTGGGCG CCGGGACCGG CATCGTCATC GATCCCAACG GTGTCTGTCT	360
GACCAACAAC CACGTGATCG CGGGCGCCAC CGACATCAAT GCGTTCAGCG TCGGCTCCGG	420
CCAAACCTAC GCGCTCGATG TGGTCGGGTA TGACCGCACC CAGGATGTCT CCGTGCTGCA	480
GCTGCGCGGT GCCGGTGGCC TGCCGTCGGC GGCGATCGGT GGCGGCGTCG CGGTTGGTGA	540
GCCCGTCTGC GCGATGGGCA ACAGCGGTGG GCAGGGCGGA ACGCCCCGTG CGGTGCTTGG	600
CAGGGTGGTC GCGCTCGGCC AAACCGTGCA GGCGTCGGAT TCGCTGACCG GTGCCGAAGA	660
GACATTGAAC GGGTTGATCC AGTTCGATGC CGCAATCCAG CCCGGTGATT CGGGCGGGCC	720
CGTCGTCAAC GGCCTAGGAC AGGTGGTCGG TATGAACACG GCCGCGTCCG ATAACCTCCA	780
GCTGTCCCAG GGTGGGCAGG GATTTCGCCAT TCCGATCGGG CAGGCGATGG CGATCGCGGG	840
CCAAATCCGA TCGGGTGGGG GGTCACCCAC CGTTCATATC GGGCCTACCG CCTTCCTCGG	900
CTTGGGTGTT GTCGACAACA ACGGCAACGG CGCACGAGTC CAACGCGTGG TCGGAAGCGC	960
TCCGGCGGCA AGTCTCGGCA TCTCCACCGG CGACGTGATC ACCGCGGTCT ACGGCGCTCC	1020
GATCAACTCG GCCACCGCGA TGGCGGACGC GCTTAACGGG CATCATCCCG GTGACGTCAT	1080
CTCGGTGAAC TGGCAAACCA AGTCGGGCGG CACGCGTACA GGGAACGTGA CATTGGCCGA	1140
GGGACCCCCG GCCTGATTTG TCGCGGATAC CACCCGCCGG CCGGCCAATT GGATTGGCGC	1200
CAGCCGTGAT TGCCGCGTGA GCCCCGAGT TCCGTCTCCC GTGCGCGTGG CATTGTGGAA	1260
GCAATGAACG AGGCAGAACA CAGCGTTGAG CACCCTCCCG TGCAGGGCAG TTACGTCGAA	1320
GGCGGTGTGG TCGAGCATCC GGATGCCAAG GACTTCGGCA GCGCCGCCGC CCTGCCCGCC	1380
GATCCGACCT GGTTTAAGCA CGCCGTCTTC TACGAGGTGC TGGTCCGGGC GTTCTTCGAC	1440
GCCAGCGCGG ACGGTTCCGN CGATCTGCGT GGAATCATCG ATCGCCTCGA CTACCTGCAG	1500
TGGCTTGGCA TCGACTGCAT CTGTTGCCGC CGTTCCTACG ACTCACCGCT GCGCGACGGC	1560
GGTTACGACA TTCGCGACTT CTACAAGGTG CTGCCCCAAT TCGGCACCGT CGACGATTTT	1620
GTCGCCCTGG TCGACACCGC TCACCGGCGA GGTATCCGCA TCATCACCGA CCTGGTGATG	1680
AATCACACCT CGGAGTCGCA CCCCTGGTTT CAGGAGTCCC GCCGCGACCC AGACGGACCG	1740
TACGGTGAAT ATTACGTGTG GAGCGACACC AGCGAGCGCT ACACCGACGC CCGGATCATC	1800
TTCGTGACGA CCGAAGAGTC GAACTGGTCA TTCGATCCTG TCCGCCGACA GTTNCTACTG	1860
GCACCGATTC TT	1872

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1482 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CTTCGCCGAA ACCTGATGCC GAGGAACAGG GTGTTCCCGT GAGCCCGACG GCGTCCGACC	60
CCGCGCTCCT CGCCGAGATC AGGCAGTCGC TTGATGCGAC AAAAGGGTTG ACCAGCGTGC	120
ACGTAGCGGT CCGAACAACC GGGAAAGTCG ACAGCTTGCT GGGTATTACC AGTGCCGATG	180
TCGACGTCCG GGCCAATCCG CTCGCGGCAA AGGGCGTATG CACCTACAAC GACGAGCAGG	240
GTGTCCCGTT TCGGGTACAA GCGGACAACA TCTCGGTGAA ACTGTTGAC GACTGGAGCA	300
ATCTCGGCTC GATTTCTGAA CTGTCAACTT CACGCGTGCT CGATCCTGCC GCTGGGGTGA	360
CGCAGCTGCT GTCCGGTGTC ACGAACCTCC AAGCGCAAGG TACCGAAGTG ATAGACGGAA	420
TTTCGACCAC CAAAATCACC GGGACCATCC CCGCGAGCTC TGTCAAGATG CTTGATCCTG	480
GCGCCAAGAG TGCAAGGCCG GCGACCGTGT GGATTGCCCA GGACGGCTCG CACCACCTCG	540
TCCGAGCGAG CATCGACCTC GGATCCGGGT CGATTCAGCT CACGCAGTCG AAATGGAACG	600
AACCCGTCAA CGTCGACTAG GCCGAAGTTG CGTCGACGCG TTGCTCGAAA CGCCCTTGTTG	660
AACGGTGTCA ACGGCACCCG AAAACTGACC CCCTGACGGC ATCTGAAAAT TGACCCCTA	720
GACCGGGCGG TTGGTGGTTA TTCTTCGGTG GTTCCGGCTG GTGGGACGCG GCCGAGGTCG	780
CGGTCTTTGA GCCGGTAGCT GTCGCCTTTG AGGGCGACGA CTTCAGCATG GTGGACGAGG	840
CGGTGCATCA TGGCGGCAGC AACGACGTCG TCGCCGCCGA AAACCTCGCC CCACCGGCCG	900
AAGGCCTTAT TGGACGTGAC GATCAAGCTG GCCCGCTCAT ACCGGGAGGA CACCAGCTGG	960
AAGAAGAGGT TGGCGGCCTC GGGCTCAAAC GGAATGTAAC CGACTTCGTC AACCACCAGG	1020
AGCGGATAGC GGCCAAACCG GGTGAGTTG GCGTAGATGC GCCCGGCGTG GTGAGCCTCG	1080
GCGAACCGTG CTACCCATTC GCGGGCGGTG GCGAACAGCA CCCGATGACC GGCCTGACAC	1140
GCGCGTATCG CCAGGCCGAC CGCAAGATGA GTCTTCCCGG TGCCAGGCGG GGCCCAAAAA	1200
CACGACGTTA TCGCGGGCGG TGATGAAATC CAGGGTGCCC AGATGTGCGA TGGTGTCGCG	1260
TTTGAGGCCA CGAGCATGCT CAAAGTCGAA CTCTTCCAAC GACTTCCGAA CCGGGAAGCG	1320
GGCGGCGCGG ATGCGGCCCT CACCACCATG GGACTCCCGG GCTGACACTT CCCGCTGCAG	1380
GCAGGCGGCC AGGTATTCTT CGTGGCTCCA GTTCTCGGCG CGGGCGCGAT CGGCCAGCCG	1440
GGACACTGAC TCACGCAGGG TGGGAGCTTT CAATGCTCTT GT	1482

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 876 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GAATTCGGCA CGAGCCGGCG ATAGCTTCTG GGCCGCGGCC GACCAGATGG CTCGAGGGTT	60
CGTGCTCGGG GCCACCGCCG GCGCACCAC CCTGACCGGT GAGGGCCTGC AACACGCCGA	120
CGGTCAC TCG TTGCTGCTGG ACGCCACCAA CCCGGCGGTG GTTGCCTACG ACCCGGCCTT	180
CGCCTACGAA ATCGGCTACA TCGNGGAAAG CGGACTGGCC AGGATGTGCG GGGAGAACCC	240
GGAGAACATC TTCTTCTACA TCACCGTCTA CAACGAGCCG TACGTGCAGC CGCCGGAGCC	300
GGAGAACTTC GATCCCGAGG GCGTGCTGGG GGGTATCTAC CGNTATCACG CGGCCACCGA	360
GCAACGCACC AACAAGGNGC AGATCCTGGC CTCCGGGGTA GCGATGCCCC CGGCGCTGCG	420
GGCAGCACAG ATGCTGGCCG CCGAGTGGGA TGTCGCCGCC GACGTGTGGT CGGTGACCAG	480
TTGGGGCGAG CTAAACCGCG ACGGGGTGGT CATCGAGACC GAGAAGCTCC GCCACCCCGA	540
TCGGCCGGCG GCGTGCCCT ACGTGACGAG AGCGCTGGAG AATGCTCGGG GCCCGGTGAT	600
CGCGGTGTCG GACTGGATGC GCGCGGTCCC CGAGCAGATC CGACCGTGGG TGCCGGGCAC	660
ATACCTCACG TTGGGCACCG ACGGGTTCGG TTTTCCGAC ACTCGGCCCG CCGGTCGTCG	720
TTACTTCAAC ACCGACGCCG AATCCCAGGT TGGTCGCGGT TTTGGGAGGG GTTGGCCGGG	780
TCGACGGGTG AATATCGACC CATTGCGTGC CGGTCGTGGG CCGCCCGCCC AGTTACCCGG	840
ATTCGACGAA GGTGGGGGGT TGCGCCCGAN TAAGTT	876

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1021 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

ATCCCCCGG GCTGCAGGAA TTCGGCACGA GAGACAAAAT TCCACGCGTT AATGCAGGAA	60
CAGATTCATA ACGAATTCAC AGCGGCACAA CAATATGTCG CGATCGCGGT TTATTTCGAC	120

AGCGAAGACC TGCCGCAGTT GGCGAAGCAT TTTTACAGCC AAGCGGTCGA GGAACGAAAC	180
CATGCAATGA TGCTCGTGCA ACACCTGCTC GACCGCGACC TTCGTGTCGA AATTCCCGGC	240
GTAGACACGG TGCGAAACCA GTTCGACAGA CCCC GCGAGG CACTGGCGCT GCGGCTCGAT	300
CAGGAACGCA CAGTCACCGA CCAGGTCGGT CGGCTGACAG CGGTGGCCCG CGACGAGGGC	360
GATTTCTCTG GCGAGCAGTT CATGCAGTGG TTCTTGACAG AACAGATCGA AGAGGTGGCC	420
TTGATGGCAA CCCTGGTGCG GGTGCGCGAT CGGGCCGGGG CCAACCTGTT CGAGCTAGAG	480
AACTTCGTG CACGTGAAGT GGATGTGGCG CCGGCCGCAT CAGGCGCCCC GCACGCTGCC	540
GGGGGCCGCC TCTAGATCCC TGGGGGGGAT CAGCGAGTGG TCCCGTTCGC CCGCCCGTCT	600
TCCAGCCAGG CCTTGGTGCG GCCGGGGTGG TGAGTACCAA TCCAGGCCAC CCCGACCTCC	660
CGGNAAAAGT CGATGTCCTC GTACTCATCG ACGTTCCAGG AGTACACCGC CCGGCCCTGA	720
GCTGCCGAGC GGTCAACGAG TTGCGGATAT TCCTTTAACG CAGGCAGTGA GGGTCCCACG	780
GCGGTTGGCC CGACCGCCGT GGCCGCACTG CTGGTCAGGT ATCGGGGGGT CTTGGCGAGC	840
AACAACGTCG GCAGGAGGGG TGGAGCCCGC CGGATCCGCA GACCGGGGGG GCGAAAACGA	900
CATCAACACC GCACGGGATC GATCTGCGGA GGGGGGTGCG GGAATACCGA ACCGGTGTAG	960
GAGCGCCAGC AGTTGTTTTT CCACCAGCGA AGCGTTTTTCG GGTCATCGGN GGCNNTTAAG	1020
T	1021

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 321 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

CGTGCCGACG AACGGAAGAA CACAACCATG AAGATGGTGA AATCGATCGC CGCAGGTCTG	60
ACCGCCGCGG CTGCAATCGG CGCCGCTGCG GCCGGTGTGA CTTCGATCAT GGCTGGCGGN	120
CCGGTCGTAT ACCAGATGCA GCCGGTCGTC TTCGGCGCGC CACTGCCGTT GGACCCGGNA	180
TCCGCCCCCTG ANGTCCCGAC CGCCGCCCAG TGGACCAGNC TGCTCAACAG NCTCGNCGAT	240
CCCAACGTGT CGTTTGNGAA CAAGGGNAGT CTGGTCGAGG GNNGNATCGG NGGNANCGAG	300
GGNGNGNATC GNCGANACA A	321

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 373 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

TCTTATCGGT TCCGGTTGGC GACGGGTTTT GGGNGCGGGT GGTTAACCCG CTCGGCCAGC	60
CGATCGACGG GCGCGGAGAC GTCGACTCCG ATACTCGGCG CGCGCTGGAG CTCCAGGCGC	120
CCTCGGTGGT GNACCGGCAA GCGGTGAAGG AGCCGTTGNA GACCGGGATC AAGGCGATTG	180
ACGCGATGAC CCCGATCGGC CGCGGGCAGC GCCAGCTGAT CATCGGGGAC CGCAAGACCG	240
GCAAAAACCG CCGTCTGTGT CGGACACCAT CCTCAAACCA GCGGAAGAA CTGGGAGTCC	300
GGTGGATCCC AAGAAGCAGG TGCCTTGTG TATACGTTGG CCATCGGGCA AGAAGGGGAA	360
CTTACCATCG CCG	373

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 352 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GTGACGCCGT GATGGGATTC CTGGGCGGGG CCGGTCCGCT GGCGGTGGTG GATCAGCAAC	60
TGGTTACCCG GGTGCCGCAA GGCTGGTCGT TTGCTCAGGC AGCCGCTGTG CCGGTGGTGT	120
TCTTGACGGC CTGGTACGGG TTGGCCGATT TAGCCGAGAT CAAGGCGGGC GAATCGGTGC	180
TGATCCATGC CCGTACCGGC GGTGTGGGCA TGGCGGCTGT GCAGCTGGCT CGCCAGTGGG	240
GCGTGGAGGT TTTCGTCACC GCCAGCCGTG GNAAGTGGGA CACGCTGCGC GCCATNGNGT	300
TTGACGACGA NCCATATCGG NGATTCCNC ACATNCGAAG TTCCGANGGA GA	352

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 726 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GAAATCCGCG TTCATTCCGT TCGACCAGCG GCTGGCGATA ATCGACGAAG TGATCAAGCC	60
GCGGTTTCGCG GCGCTCATGG GTCACAGCGA GTAATCAGCA AGTTCTCTGG TATATCGCAC	120
CTAGCGTCCA GTTGCTTGCC AGATCGCTTT CGTACCGTCA TCGCATGTAC CGGTTTCGCGT	180
GCCGCACGCT CATGCTGGCG GCGTGCATCC TGGCCACGGG TGTGGCGGGT CTCGGGGTCG	240
GCGCGCAGTC CGCAGCCCAA ACCGCGCCGG TGCCCGACTA CTACTGGTGC CCGGGGCAGC	300
CTTTCGACCC CGCATGGGGG CCCAACTGGG ATCCCTACAC CTGCCATGAC GACTTCCACC	360
GCGACAGCGA CGGCCCCGAC CACAGCCGCG ACTACCCCGG ACCCATCCTC GAAGGTCCCG	420
TGCTTGACGA TCCCGGTGCT GCGCCGCCGC CCCC GGCTGC CGGTGGCGGC GCATAGCGCT	480
CGTTGACCGG GCCGCATCAG CGAATACGCG TATAAACCCG GGCGTGCCCC CGGCAAGCTA	540
CGACCCCCGG CGGGGCAGAT TTACGCTCCC GTGCCGATGG ATCGCGCCGT CCGATGACAG	600
AAAATAGGCG ACGGTTTTTG CAACCGCTTG GAGGACGCTT GAAGGGAACC TGTCATGAAC	660
GGCGACAGCG CCTCCACCAT CGACATCGAC AAGGTTGTTA CCCGCACACC CGTTCCCGCG	720
ATCGTG	726

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 580 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

CGCGACGACG ACGAACGTCG GGCCCACCAC CGCCTATGCG TTGATGCAGG CGACCGGGAT	60
GGTCGCCGAC CATATCCAAG CATGCTGGGT GCCCACTGAG CGACCTTTTG ACCAGCCGGG	120
CTGCCCCGATG GCGGCCCCGT GAAGTCATTG CGCCGGGGCT TGTGCACCTG ATGAACCCGA	180
ATAGGGAACA ATAGGGGGGT GATTTGGCAG TTCAATGTCG GGTATGGCTG GAAATCCAAT	240
GGCGGGGCAT GCTCGGCGCC GACCAGGCTC GCGCAGGCGG GCCAGCCCGA ATCTGGAGGG	300
AGCACTCAAT GCGGCGCATG AAGCCCCGGA CCGGCGACGG TCCTTTGGAA GCAACTAAGG	360
AGGGGCGCGG CATTGTGATG CGAGTACCAC TTGAGGGTGG CGGTGCGCTG GTCGTCGAGC	420
TGACACCCGA CGAAGCCGCC GCACTGGGTG ACGAACTCAA AGGCGTTACT AGCTAAGACC	480
AGCCCAACGG CGAATGGTCG GCGTTACGCG CACACCTTCC GGTAGATGTC CAGTGTCTGC	540
TCGGCGATGT ATGCCCAGGA GAACTCTTGG ATACAGCGCT	580

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 160 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

AACGGAGGCG CCGGGGGTTT TGGCGGGGCC GGGGCGGTCG GCGGCAACGG CGGGGCCGGC	60
GGTACCGCCG GGTGTGTCGG TGTCGGCGGG GCCGGTGGGG CCGGAGGCAA CGGCATCGCC	120
GGTGTCACGG GTACGTCGGC CAGCACACCG GGTGGATCCG	160

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 272 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

GACACCGATA CGATGGTGAT GTACGCCAAC GTTGTGACA CGCTCGAGGC GTTCACGATC	60
CAGCGCACAC CCGACGGCGT GACCATCGGC GATGCGGCCC CGTTCGCGGA GGCGGCTGCC	120
AAGGCGATGG GAATCGACAA GCTGCGGGTA ATTCATACCG GAATGGACCC CGTCGTCGCT	180
GAACGCGAAC AGTGGGACGA CGGCAACAAC ACGTTGGCGT TGGCGCCCGG TGTCGTTGTC	240
GCCTACGAGC GCAACGTACA GACCAACGCC CG	272

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 317 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

GCAGCCGGTG GTTCTCGGAC TATCTGCGCA CGGTGACGCA GCGCGACGTG CGCGAGCTGA	60
AGCGGATCGA GCAGACGGAT CGCCTGCCGC GGTTTCATGCG CTACCTGGCC GCTATCACCG	120

CGCAGGAGCT GAACGTGGCC GAAGCGGCGC GGGTCATCGG GGTCGACGCG GGGACGATCC 180
 GTTCGGATCT GGCCTGGTTC GAGACGGTCT ATCTGGTACA TCGCCTGCCC GCCTGGTCGC 240
 GGAATCTGAC CGCGAAGATC AAGAAGCGGT CAAAGATCCA CGTCGTCGAC AGTGGCTTCG 300
 CGGCCTGGTT GCGCGGG 317

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 182 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GATCGTGGAG CTGTCGATGA ACAGCGTTGC CGGACGCGCG GCGGCCAGCA CGTCGGTGTA 60
 GCAGCGCCGG ACCACCTCGC CCGTGGGCAG CATGGTGATG ACCACGTCGG CCTCGGCCAC 120
 CGCTTCGGGC GCGCTACGAA ACACCGCGAC ACCGTGCGCG GCGGCGCCGG ACGCCGCCGT 180
 GG 182

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 308 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

GATCGCGAAG TTTGGTGAGC AGGTGGTCGA CGCGAAAGTC TGGGCGCCTG CGAAGCGGGT 60
 CGGCGTTCAC GAGGCGAAGA CACGCCTGTC CGAGCTGCTG CGGCTCGTCT ACGGCGGGCA 120
 GAGGTTGAGA TTGCCCCCG CGGCGAGCCG GTAGCAAAGC TTGTGCCGCT GCATCCTCAT 180
 GAGACTCGGC GGTTAGGCAT TGACCATGGC GTGTACCGCG TGCCCGACGA TTTGGACGCT 240
 CCGTTGTTCAG ACGACGTGCT CGAACGCTTT CACCGGTGAA GCGCTACCTC ATCGACACCC 300
 ACGTTTGG 308

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 267 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

CCGACGACGA GCAACTCACG TGGATGATGG TCGGCAGCGG CATTGAGGAC GGAGAGAATC	60
CGGCCGAAGC TGCCGCGCGG CAAGTGCTCA TAGTGACCGG CCGTAGAGGG CTCCCCCGAT	120
GGCACC GGAC TATTCTGGTG TGCCGCTGGC CGGTAAGAGC GGGTAAAAGA ATGTGAGGGG	180
ACACGATGAG CAATCACACC TACCGAGTGA TCGAGATCGT CGGGACCTCG CCCGACGGCG	240
TCGACGCGGC AATCCAGGGC GGTCTGG	267

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1539 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

CTCGTGCCGA AAGAATGTGA GGGGACACGA TGAGCAATCA CACCTACCGA GTGATCGAGA	60
TCGTGCGGAC CTCGCCCCGAC GCGGTCGACG CGGCAATCCA GGGCGGTCTG GCCCAGAGCTG	120
CGCAGACCAT GCGCGCGCTG GACTGGTTCG AAGTACAGTC AATTCGAGGC CACCTGGTCTG	180
ACGGAGCGGT CGCGCACTTC CAGGTGACTA TGAAAGTCGG CTTCCGCTGG AGGATTCCTG	240
AACCTTCAAG CGCGCCGAT AACTGAGGTG CATCATTAAG CGACTTTTCC AGAACATCCT	300
GACGCGCTCG AAACGCGGTT CAGCCGACGG TGGCTCCGCC GAGGCGCTGC CTCCAAAATC	360
CCTGCGACAA TTCGTGCGCG GCGCCTACAA GGAAGTCGGT GCTGAATTCG TCGGGTATCT	420
GGTCGACCTG TGTGGGCTGC AGCCGGACGA AGCGGTGCTC GACGTCGGCT GCGGCTCGGG	480
GCGGATGGCG TTGCCGCTCA CCGGCTATCT GAACAGCGAG GGACGCTACG CCGGCTTCGA	540
TATCTCGCAG AAAGCCATCG CGTGGTGCCA GGAGCACATC ACCTCGGCGC ACCCCAACCT	600
CCAGTTCGAG GTCTCCGACA TCTACAACTC GCTGTACAAC CCGAAAGGGA AATACCAGTC	660
ACTAGACTTT CGCTTTCCAT ATCCGGATGC GTCGTTTCGAT GTGGTGTTTC TTACCTCGGT	720
GTTCACCCAC ATGTTTCCGC CGGACGTGGA GCACTATCTG GACGAGATCT CCCGCGTGCT	780
GAAGCCCGGC GGACGATGCC TGTGCACGTA CTTCTTGCTC AATGACGAGT CGTTAGCCCA	840
CATCGCGGAA GGAAAGAGTG CGCACAACTT CCAGCATGAG GGACCGGGTT ATCGGACAAT	900

CCACAAGAAG CGGCCCCGAAG AAGCAATCGG CTTGCCGGAG ACCTTCGTCA GGGATGTCTA	960
TGGCAAGTTC GGCCTCGCCG TGCACGAACC ATTGCACTAC GGCTCATGGA GTGGCCGGGA	1020
ACCACGCCTA AGCTTCCAGG ACATCGTCAT CGCGACCAA ACCGCGAGCT AGGTCGGCAT	1080
CCGGGAAGCA TCGCGACACC GTGGCGCCGA GCGCCGCTGC CGGCAGGCCG ATTAGGCGGG	1140
CAGATTAGCC CGCCGCGGCT CCCGGCTCCG AGTACGGCGC CCCGAATGGC GTCACCGGCT	1200
GGTAACCACG CTTGCGCGCC TGGGCGGCGG CCTGCCGGAT CAGGTGGTAG ATGCCGACAA	1260
AGCCTGCGTG ATCGGTCATC ACCAACGGTG ACAGCAGCCG GTTGTGCACC AGCGCGAACG	1320
CCACCCCGGT CTCCGGGTCT GTCCAGCCGA TCGAGCCGCC CAAGCCCACA TGACCAAACC	1380
CCGGCATCAC GTTGCCGATC GGCATACCGT GATAGCCAAG ATGAAAATTT AAGGGCACCA	1440
ATAGATTTTCG ATCCGGCAGA ACTTGCCGTC GGTGCGGGT CAGGCCCCGTG ACCAGCTCCC	1500
GCGACAAGAA CCGTATGCCG TCGATCTCGC CTCGTGCCG	1539

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 851 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

CTGCAGGGTG GCGTGGATGA GCGTCACCGC GGGGCAGGCC GAGCTGACCG CCGCCCAGGT	60
CCGGGTTGCT GCGGCGGCCT ACGAGACGGC GTATGGGCTG ACGGTGCCCC CGCCGGTGAT	120
CGCCGAGAAC CGTGCTGAAC TGATGATTCT GATAGCGACC AACCTCTTGG GGCAAAACAC	180
CCCGGCGATC GCGGTCAACG AGGCCGAATA CGGCGAGATG TGGGCCCAAG ACGCCGCCGC	240
GATGTTTGGC TACGCCGCGG CGACGGCGAC GGCGACGGCG ACGTTGCTGC CGTTCGAGGA	300
GGCGCCGGAG ATGACCAGCG CGGGTGGGCT CCTCGAGCAG GCCGCCGCGG TCGAGGAGGC	360
CTCCGACACC GCCGCGGCGA ACCAGTTGAT GAACAATGTG CCCAGGCGC TGAAACAGTT	420
GGCCCAGCCC ACGCAGGGCA CCACGCCTTC TTCCAAGCTG GGTGGCCTGT GGAAGACGGT	480
CTCGCCGCAT CGGTCGCCGA TCAGCAACAT GGTGTCGATG GCCAACAACC ACATGTCGAT	540
GACCAACTCG GGTGTGTCGA TGACCAACAC CTTGAGCTCG ATGTTGAAGG GCTTTGCTCC	600
GGCGGCGGCC GCCCAGGCCG TGCAAACCGC GGCGCAAAAC GGGGTCCGGG CGATGAGCTC	660
GCTGGGCAGC TCGCTGGGTT CTTGCGGTCT GGGCGGTGGG GTGGCCGCCA ACTTGGGTGC	720
GGCGGCCTCG GTACGGTATG GTCACCGGGA TGGCGGAAAA TATGCANAGT CTGGTCGGCG	780

GAACGGTGGT CCGGCGTAAG GTTTACCCCC GTTTTCTGGA TCGGTGAAC TTCGTCAACG 840
 GAAACAGTTA C 851

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 254 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GATCGATCGG GCGGAAATTT GGACCAGATT CGCCTCCGGC GATAACCCAA TCAATCGAAC 60
 CTAGATTTAT TCCGTCCAGG GGCCCGAGTA ATGGCTCGCA GGAGAGGAAC CTTACTGCTG 120
 CGGGCACCTG TCGTAGGTCC TCGATACGGC GGAAGGCGTC GACATTTTCC ACCGACACCC 180
 CCATCCAAAC GTTCGAGGGC CACTCCAGCT TGTGAGCGAG GCGACGCAGT CGCAGGCTGC 240
 GCTTGGTCAA GATC 254

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1227 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

GATCCTGACC GAAGCGGCCG CCGCCAAGGC GAAGTCGCTG TTGGACCAGG AGGGACGGGA 60
 CGATCTGGCG CTGCGGATCG CGGTTAGCC GGGGGGGTGC GCTGGATTGC GCTATAACCT 120
 TTTCTTCGAC GACCGGACGC TGGATGGTGA CCAAACCGCG GAGTTCGGTG GTGTCAGGTT 180
 GATCGTGGAC CGGATGAGCG CGCCGTATGT GGAAGGCGCG TCGATCGATT TCGTCGACAC 240
 TATTGAGAAG CAAGGTTTAC CATCGACAAT CCCAACGCCA CCGGCTCCTG CGCGTGC GGG 300
 GATTTCGTTCA ACTGATAAAA CGCTAGTACG ACCCCGCGGT GCGCAACACG TACGAGCACA 360
 CCAAGACCTG ACCGCGCTGG AAAAGCAACT GAGCGATGCC TTGCACCTGA CCGCGTGGCG 420
 GGCCGCCGGC GGCAGGTGTC ACCTGCATGG TGAACAGCAC CTGGGCCTGA TATTGCGACC 480
 AGTACACGAT TTTGTGATC GAGGTCACTT CGACCTGGGA GAACTGCTTG CGGAACGCGT 540
 CGCTGCTCAG CTTGGCCAAG GCCTGATCGG AGCGCTTGTC GCGCACGCCG TCGTGGATAC 600

CGCACAGCGC ATTGCGAACG ATGGTGTCCA CATCGCGGTT CTCCAGCGCG TTGAGGTATC	660
CCTGAATCGC GGTTTTGGCC GGTCCCTCCG AGAATGTGCC TGCCGTGTTG GCTCCGTTGG	720
TGCGGACCCC GTATATGATC GCCGCCGTCA TAGCCGACAC CAGCGCGAGG GCTACCACAA	780
TGCCGATCAG CAGCCGCTTG TGCCGTGCTT TCGGGTAGGA CACCTGCGGC GGCACGCCGG	840
GATATGCGGC GGGCGGCAGC GCCGCGTCGT CTGCCGGTCC CGGGGCGAAG GCCGGTTCGG	900
CGGCGCCGAG GTCGTGGGGG TAGTCCAGGG CTTGGGGTTC GTGGGATGAG GGCTCGGGGT	960
ACGGCGCCGG TCCGTTGGTG CCGACACCGG GGTTCGGCGA GTGGGGACCG GGCATTGTGG	1020
TTCTCCTAGG GTGGTGGACG GGACCAGCTG CTAGGGCGAC AACCGCCCGT CGCGTCAGCC	1080
GGCAGCATCG GCAATCAGGT GAGCTCCCTA GGCAGGCTAG CGCAACAGCT GCCGTCAGCT	1140
CTCAACCGCA CGGGGCGGGC CGCGGCGCCG ATAATGTTGA AAGACTAGGC AACCTTAGGA	1200
ACGAAGGACG GAGATTTTGT GACGATC	1227

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 181 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

GCGGTGTCGG CGGATCCGGC GGGTGGTTGA ACGGCAACGG CGGGGCCGGC GGGGCCGGCG	60
GGACCGGCGC TAACGGTGGT GCCGGCGGCA ACGCCTGGTT GTTCGGGGCC GGCGGGTCCG	120
GCGGNGCCGG CACCAATGGT GGNGTCGGCG GGTCCGGCGG ATTTGTCTAC GGCAACGGCG	180
G	181

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 290 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GCGGTGTCGG CGGATCCGGC GGGTGGTTGA ACGGCAACGG CGGTGTCGGC GGCCGGGGCG	60
GCGACGGCGT CTTTGCCGGT GCCGGCGGCC AGGGCGGCCT CGGTGGGCAG GGCGGCAATG	120

GCGGCGGCTC CACCGGCGGC AACGGCGGTC TTGGCGGCGC GGGCGGTGGC GGAGGCAACG 180
CCCCGGACGG CGGCTTCGGT GGCAACGGCG GTAAGGGTGG CCAGGGCGGN ATTGGCGGCG 240
GCACTCAGAG CGCGACCGGC CTCGGNGGTG ACGGCGGTGA CGGCGGTGAC 290

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 34 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

GATCCAGTGG CATGGNGGGT GTCAGTGGAA GCAT 34

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 155 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

GATCGCTGCT CGTCCCCCCC TTGCCGCCGA CGCCACCGGT CCCACCGTTA CCGAACAAGC 60
TGGCGTGGTC GCCAGCACCC CCGGCACCGC CGACGCCGGA GTCGAACAAT GGCACCGTCG 120
TATCCCCACC ATTGCCGCCG GNCCCACCGG CACCG 155

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

ATGGCGTTCA CGGGGCGCCG GGGACCGGGC AGCCCGGNGG GGCCGGGGGG TGG 53

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 132 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

GATCCACCGC GGGTGCAGAC GGTGCCCCGCG GCGCCACCCC GACCAGCGGC GGCAACGGCG	60
GCACCGGCGG CAACGGCGCG AACGCCACCG TCGTCGGNGG GGCCGGCGGG GCCGGCGGCA	120
AGGGCGGCAA CG	132

(2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 132 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

GATCGGCGGC CGGNACGGNC GGGGACGGCG GCAAGGGCGG NAACGGGGGC GCCGNAGCCA	60
CCNGCCAAGA ATCCTCCGNG TCCNCCAATG GCGCGAATGG CGGACAGGGC GGCAACGGCG	120
GCANCGGCGG CA	132

(2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 702 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

CGGCACGAGG ATCGGTACCC CGCGGCATCG GCAGCTGCCG ATTCGCCGGG TTTCCCCACC	60
CGAGGAAAGC CGCTACCAGA TGGCGCTGCC GAAGTAGGGC GATCCGTTCG CGATGCCGGC	120
ATGAACGGGC GGCATCAAAT TAGTGCAGGA ACCTTTCAGT TTAGCGACGA TAATGGCTAT	180
AGCACTAAGG AGGATGATCC GATATGACGC AGTCGCAGAC CGTGACGGTG GATCAGCAAG	240
AGATTTTGAA CAGGGCCAAC GAGGTGGAGG CCCCATGGC GGACCCACCG ACTGATGTCC	300
CCATCACACC GTGCGAACTC ACGGNGGNTA AAAACGCCGC CCAACAGNTG GTNTTGTCCG	360

CCGACAACAT GCGGGAATAC CTGGCGGCCG GTGCCAAAGA GCGGCAGCGT CTGGCGACCT	420
CGCTGCGCAA CGCGGCCAAG GNGTATGGCG AGGTTGATGA GGAGGCTGCG ACCGCGCTGG	480
ACAACGACGG CGAAGGAACT GTGCAGGCAG AATCGGCCGG GGCCGTCGGA GGGGACAGTT	540
CGGCCGAACT AACCGATACG CCGAGGGTGG CCACGGCCGG TGAACCCAAC TTCATGGATC	600
TCAAAGAAGC GGCAAGGAAG CTCGAAACGG GCGACCAAGG CGCATCGCTC GCGCACTGNG	660
GGGATGGGTG GAACACTTNC ACCCTGACGC TGCAAGGCGA CG	702

(2) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 298 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

GAAGCCGCAG CGCTGTCGGG CGACGTGGCG GTCAAAGCGG CATCGCTCGG TGGCGGTGGA	60
GGCGGCGGGG TGCCGTCGGC GCCGTTGGGA TCCGCGATCG GGGGCGCCGA ATCGGTGCGG	120
CCCGCTGGCG CTGGTGACAT TGCCGGCTTA GGCCAGGGAA GGGCCGGCGG CGGCGCCGCG	180
CTGGGCGGCG GTGGCATGGG AATGCCGATG GGTGCCGCGC ATCAGGGACA AGGGGGCGCC	240
AAGTCCAAGG GTTCTCAGCA GGAAGACGAG GCGCTCTACA CCGAGGATCC TCGTGCCG	298

(2) INFORMATION FOR SEQ ID NO:45:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1058 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

CGGCACGAGG ATCGAATCGC GTCGCCGGGA GCACAGCGTC GCACTGCACC AGTGGAGGAG	60
CCATGACCTA CTCGCCGGGT AACCCCGGAT ACCCGCAAGC GCAGCCCGCA GGCTCCTACG	120
GAGGCGTCAC ACCCTCGTTC GCCCACGCCG ATGAGGGTGC GAGCAAGCTA CCGATGTACC	180
TGAACATCGC GGTGGCAGTG CTCGGTCTGG CTGCGTACTT CGCCAGCTTC GGCCCAATGT	240
TCACCCCTCAG TACCGAACTC GGGGGGGGTG ATGGCGCAGT GTCCGGTGAC ACTGGGCTGC	300
CGGTGCGGGT GGCTCTGCTG GCTGCGCTGC TTGCCGGGGT GGTTCCTGGTG CCTAAGGCCA	360

AGAGCCATGT GACGGTAGTT GCGGTGCTCG GGGTACTCGG CGTATTTCTG ATGGTCTCGG	420
CGACGTTTAA CAAGCCCAGC GCCTATTCGA CCGGTGCGG ATTGTGGGT GTGTTGGCTT	480
TCATCGTGTT CCAGGCGGTT GCGGCAGTCC TGGCGCTCTT GGTGGAGACC GGCGCTATCA	540
CCGCGCCGGC GCCGCGGCCC AAGTTCGACC CGTATGGACA GTACGGGCGG TACGGGCAGT	600
ACGGGCAGTA CGGGGTGAG CCGGGTGGGT ACTACGGTCA GCAGGGTGCT CAGCAGGCCG	660
CGGGACTGCA GTCGCCCCGC CCGCAGCAGT CTCCGCAGCC TCCCGGATAT GGGTCGCAGT	720
ACGGCGGCTA TTCGTCCAGT CCGAGCCAAT CGGGCAGTGG ATACACTGCT CAGCCCCCGG	780
CCCAGCCGCC GGCGCAGTCC GGGTCGCAAC AATCGCACCA GGGCCCATCC ACGCCACCTA	840
CCGGCTTTCC GAGCTTCAGC CCACCACCAC CGGTCAGTGC CGGGACGGGG TCGCAGGCTG	900
GTTTCGGCTCC AGTCAACTAT TCAAACCCCA GCGGGGGCGA GCAGTCGTCG TCCCCCGGGG	960
GGGCGCCGGT CTAACCGGGC GTTCCCGCGT CCGGTCGCGC GTGTGCGCGA AGAGTGAACA	1020
GGGTGTCAGC AAGCGCGGAC GATCCTCGTG CCGAATTC	1058

(2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 327 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

CGGCACGAGA GACCGATGCC GCTACCCTCG CGCAGGAGGC AGGTAATTTT GAGCGGATCT	60
CCGGCGACCT GAAAACCCAG ATCGACCAGG TGGAGTCGAC GGCAGGTTTC TTGCAGGGCC	120
AGTGGCGCGG CGCGGCGGGG ACGGCCGCCC AGGCCGCGGT GGTGCGCTTC CAAGAAGCAG	180
CCAATAAGCA GAAGCAGGAA CTCGACGAGA TCTCGACGAA TATTCGTCAG GCCGGCGTCC	240
AATACTCGAG GGCCGACGAG GAGCAGCAGC AGGCGCTGTC CTCGCAAATG GGCTTCTGAC	300
CCGCTAATAC GAAAAGAAAC GGAGCAA	327

(2) INFORMATION FOR SEQ ID NO:47:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 170 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

CGGTCGCGAT GATGGCGTTG TCGAACGTGA CCGATTCTGT ACCGCCGTCG TTGAGATCAA	60
CCAACAACGT GTTGGCGTCG GCAAATGTGC CGNACCCGTG GATCTCGGTG ATCTTGTCT	120
TCTTCATCAG GAAGTGCACA CCGGCCACCC TGCCCTCGGN TACCTTTCGG	170

(2) INFORMATION FOR SEQ ID NO:48:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 127 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

GATCCGGCGG CACGGGGGGT GCCGGCGGCA GCACCGCTGG CGCTGGCGGC AACGGCGGGG	60
CCGGGGGTGG CGGCGGAACC GGTGGGTTGC TCTTCGGCAA CGGCGGTGCC GGCGGGCAGC	120
GGGCCGT	127

(2) INFORMATION FOR SEQ ID NO:49:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 81 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

CGGCGGCAAG GGCGGCACCG CCGGCAACGG GAGCGGCGCG GCCGGCGGCA ACGGCGGCAA	60
CGGCGGCTCC GGCCTCAACG G	81

(2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 149 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

GATCAGGGCT GGCCGGCTCC GGCCAGAAGG GCGGTAACGG AGGAGCTGCC GGATTGTTTG	60
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GCAACGGCGG GGCCGGNGGT GCCGGCGCGT CCAACCAAGC CGGTAACGGC GGNGCCGGCG 120
 GAAACGGTGG TGCCGGTGGG CTGATCTGG 149

(2) INFORMATION FOR SEQ ID NO:51:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 355 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

CGGCACGAGA TCACACCTAC CGAGTGATCG AGATCGTCGG GACCTCGCCC GACGGTGTCTG 60
 ACGCGGNAAT CCAGGGCGGT CTGGCCCGAG CTGCGCAGAC CATGCGCGCG CTGGACTGGT 120
 TCGAAGTACA GTCAATTCGA GGCCACCTGG TCGACGGAGC GGTGCGGCAC TTCCAGGTGA 180
 CTATGAAAGT CGGCTTCCGC CTGGAGGATT CCTGAACCTT CAAGCGCGGC CGATAACTGA 240
 GGTGCATCAT TAAGCGACTT TTCCAGAACA TCCTGACGCG CTCGAAACGC GGTTGAGCCG 300
 ACGGTGGCTC CGCCGAGGCG CTGCCTCCAA AATCCCTGCG ACAATTGCTC GGCGG 355

(2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 999 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

ATGCATCACC ATCACCATCA CATGCATCAG GTGGACCCCA ACTTGACACG TCGCAAGGGA 60
 CGATTGGCGG CACTGGCTAT CGCGGCGATG GCCAGCGCCA GCCTGGTGAC CGTTGCGGTG 120
 CCCGCGACCG CCAACGCCGA TCCGGAGCCA GCGCCCCCGG TACCCACAAC GGCCGCCTCG 180
 CCGCCGTCGA CCGCTGCAGC GCCACCCGCA CCGGCGACAC CTGTTGCCCC CCCACCACCG 240
 GCCGCCGCCA ACACGCCGAA TGCCAGCCG GCGGATCCCA ACGCAGCACC TCCGCCGGCC 300
 GACCCGAACG CACCGCCGCC ACCTGTCATT GCCCCAAACG CACCCCAACC TGTCCGGATC 360
 GACAACCCGG TTGGAGGATT CAGCTTCGCG CTGCCTGCTG GCTGGGTGGA GTCTGACGCC 420
 GCCCCTTCG ACTACGGTTC AGCACTCCTC AGCAAAACCA CCGGGGACCC GCCATTTCCC 480
 GGACAGCCGC CGCCGGTGGC CAATGACACC CGTATCGTGC TCGGCCGGCT AGACCAAAAG 540


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CTTTACGCCA GCGCCGAAGC CACCGACTCC AAGGCCGCGG CCCGGTTGGG CTCGGACATG      600
GGTGAGTTCT ATATGCCCTA CCCGGGCACC CGGATCAACC AGGAAACCGT CTCGCTCGAC      660
GCCAACGGGG TGTCTGGAAG CGCGTCGTAT TACGAAGTCA AGTTCAGCGA TCCGAGTAAG      720
CCGAACGGCC AGATCTGGAC GGGCGTAATC GGCTCGCCCG CGGCGAACGC ACCGGACGCC      780
GGGCCCCCTC AGCGCTGGTT TGTGGTATGG CTCGGGACCG CCAACAACCC GGTGGACAAG      840
GGCGCGGCCA AGGCGCTGGC CGAATCGATC CGGCCTTTGG TCGCCCCGCC GCCGGCGCCG      900
GCACCGGCTC CTGCAGAGCC CGCTCCGGCG CCGGCGCCCG CCGGGGAAGT CGCTCCTACC      960
CCGACGACAC CGACACCGCA GCGGACCTTA CCGGCCTGA                               999

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(2) INFORMATION FOR SEQ ID NO:53:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 332 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

```

Met His His His His His Met His Gln Val Asp Pro Asn Leu Thr
1          5          10          15
Arg Arg Lys Gly Arg Leu Ala Ala Leu Ala Ile Ala Ala Met Ala Ser
          20          25          30
Ala Ser Leu Val Thr Val Ala Val Pro Ala Thr Ala Asn Ala Asp Pro
          35          40          45
Glu Pro Ala Pro Pro Val Pro Thr Thr Ala Ala Ser Pro Pro Ser Thr
          50          55          60
Ala Ala Ala Pro Pro Ala Pro Ala Thr Pro Val Ala Pro Pro Pro Pro
          65          70          75          80
Ala Ala Ala Asn Thr Pro Asn Ala Gln Pro Gly Asp Pro Asn Ala Ala
          85          90          95
Pro Pro Pro Ala Asp Pro Asn Ala Pro Pro Pro Pro Val Ile Ala Pro
          100          105          110
Asn Ala Pro Gln Pro Val Arg Ile Asp Asn Pro Val Gly Gly Phe Ser
          115          120          125
Phe Ala Leu Pro Ala Gly Trp Val Glu Ser Asp Ala Ala His Phe Asp
          130          135          140
Tyr Gly Ser Ala Leu Leu Ser Lys Thr Thr Gly Asp Pro Pro Phe Pro
          145          150          155          160
Gly Gln Pro Pro Pro Val Ala Asn Asp Thr Arg Ile Val Leu Gly Arg
          165          170          175

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Leu Asp Gln Lys Leu Tyr Ala Ser Ala Glu Ala Thr Asp Ser Lys Ala
 180 185 190
 Ala Ala Arg Leu Gly Ser Asp Met Gly Glu Phe Tyr Met Pro Tyr Pro
 195 200 205
 Gly Thr Arg Ile Asn Gln Glu Thr Val Ser Leu Asp Ala Asn Gly Val
 210 215 220
 Ser Gly Ser Ala Ser Tyr Tyr Glu Val Lys Phe Ser Asp Pro Ser Lys
 225 230 235 240
 Pro Asn Gly Gln Ile Trp Thr Gly Val Ile Gly Ser Pro Ala Ala Asn
 245 250 255
 Ala Pro Asp Ala Gly Pro Pro Gln Arg Trp Phe Val Val Trp Leu Gly
 260 265 270
 Thr Ala Asn Asn Pro Val Asp Lys Gly Ala Ala Lys Ala Leu Ala Glu
 275 280 285
 Ser Ile Arg Pro Leu Val Ala Pro Pro Pro Ala Pro Ala Pro Ala Pro
 290 295 300
 Ala Glu Pro Ala Pro Ala Pro Ala Pro Ala Gly Glu Val Ala Pro Thr
 305 310 315 320
 Pro Thr Thr Pro Thr Pro Gln Arg Thr Leu Pro Ala
 325 330

(2) INFORMATION FOR SEQ ID NO:54:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

Asp Pro Val Asp Ala Val Ile Asn Thr Thr Xaa Asn Tyr Gly Gln Val
 1 5 10 15
 Val Ala Ala Leu
 20

(2) INFORMATION FOR SEQ ID NO:55:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 15 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

Ala Val Glu Ser Gly Met Leu Ala Leu Gly Thr Pro Ala Pro Ser
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Ala Ala Met Lys Pro Arg Thr Gly Asp Gly Pro Leu Glu Ala Ala Lys
1 5 10 15
Glu Gly Arg

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

Tyr Tyr Trp Cys Pro Gly Gln Pro Phe Asp Pro Ala Trp Gly Pro
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

Asp Ile Gly Ser Glu Ser Thr Glu Asp Gln Gln Xaa Ala Val
1 5 10

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

Ala Glu Glu Ser Ile Ser Thr Xaa Glu Xaa Ile Val Pro
1 5 10

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

Asp Pro Glu Pro Ala Pro Pro Val Pro Thr Ala Ala Ala Ala Pro Pro
1 5 10 15

Ala

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

Ala Pro Lys Thr Tyr Xaa Glu Glu Leu Lys Gly Thr Asp Thr Gly
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

```

Asp Pro Ala Ser Ala Pro Asp Val Pro Thr Ala Ala Gln Gln Thr Ser
1           5           10           15
Leu Leu Asn Asn Leu Ala Asp Pro Asp Val Ser Phe Ala Asp
          20           25           30

```

(2) INFORMATION FOR SEQ ID NO:63:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 187 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

```

Thr Gly Ser Leu Asn Gln Thr His Asn Arg Arg Ala Asn Glu Arg Lys
1           5           10           15
Asn Thr Thr Met Lys Met Val Lys Ser Ile Ala Ala Gly Leu Thr Ala
          20           25           30
Ala Ala Ala Ile Gly Ala Ala Ala Gly Val Thr Ser Ile Met Ala
          35           40           45
Gly Gly Pro Val Val Tyr Gln Met Gln Pro Val Val Phe Gly Ala Pro
          50           55           60
Leu Pro Leu Asp Pro Ala Ser Ala Pro Asp Val Pro Thr Ala Ala Gln
          65           70           75           80
Leu Thr Ser Leu Leu Asn Ser Leu Ala Asp Pro Asn Val Ser Phe Ala
          85           90           95
Asn Lys Gly Ser Leu Val Glu Gly Gly Ile Gly Gly Thr Glu Ala Arg
          100          105          110
Ile Ala Asp His Lys Leu Lys Lys Ala Ala Glu His Gly Asp Leu Pro
          115          120          125
Leu Ser Phe Ser Val Thr Asn Ile Gln Pro Ala Ala Ala Gly Ser Ala
          130          135          140
Thr Ala Asp Val Ser Val Ser Gly Pro Lys Leu Ser Ser Pro Val Thr
          145          150          155          160
Gln Asn Val Thr Phe Val Asn Gln Gly Gly Trp Met Leu Ser Arg Ala
          165          170          175
Ser Ala Met Glu Leu Leu Gln Ala Ala Gly Xaa
          180          185

```

(2) INFORMATION FOR SEQ ID NO:64:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 148 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

```

Asp Glu Val Thr Val Glu Thr Thr Ser Val Phe Arg Ala Asp Phe Leu
1          5          10          15
Ser Glu Leu Asp Ala Pro Ala Gln Ala Gly Thr Glu Ser Ala Val Ser
          20          25          30
Gly Val Glu Gly Leu Pro Pro Gly Ser Ala Leu Leu Val Val Lys Arg
          35          40          45
Gly Pro Asn Ala Gly Ser Arg Phe Leu Leu Asp Gln Ala Ile Thr Ser
          50          55          60
Ala Gly Arg His Pro Asp Ser Asp Ile Phe Leu Asp Asp Val Thr Val
          65          70          75          80
Ser Arg Arg His Ala Glu Phe Arg Leu Glu Asn Asn Glu Phe Asn Val
          85          90          95
Val Asp Val Gly Ser Leu Asn Gly Thr Tyr Val Asn Arg Glu Pro Val
          100          105          110
Asp Ser Ala Val Leu Ala Asn Gly Asp Glu Val Gln Ile Gly Lys Leu
          115          120          125
Arg Leu Val Phe Leu Thr Gly Pro Lys Gln Gly Glu Asp Asp Gly Ser
          130          135          140
Thr Gly Gly Pro
          145

```

(2) INFORMATION FOR SEQ ID NO:65:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 230 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

```

Thr Ser Asn Arg Pro Ala Arg Arg Gly Arg Arg Ala Pro Arg Asp Thr
1          5          10          15
Gly Pro Asp Arg Ser Ala Ser Leu Ser Leu Val Arg His Arg Arg Gln
          20          25          30

```

Gln Arg Asp Ala Leu Cys Leu Ser Ser Thr Gln Ile Ser Arg Gln Ser
 35 40 45
 Asn Leu Pro Pro Ala Ala Gly Gly Ala Ala Asn Tyr Ser Arg Arg Asn
 50 55 60
 Phe Asp Val Arg Ile Lys Ile Phe Met Leu Val Thr Ala Val Val Leu
 65 70 75 80
 Leu Cys Cys Ser Gly Val Ala Thr Ala Ala Pro Lys Thr Tyr Cys Glu
 85 90 95
 Glu Leu Lys Gly Thr Asp Thr Gly Gln Ala Cys Gln Ile Gln Met Ser
 100 105 110
 Asp Pro Ala Tyr Asn Ile Asn Ile Ser Leu Pro Ser Tyr Tyr Pro Asp
 115 120 125
 Gln Lys Ser Leu Glu Asn Tyr Ile Ala Gln Thr Arg Asp Lys Phe Leu
 130 135 140
 Ser Ala Ala Thr Ser Ser Thr Pro Arg Glu Ala Pro Tyr Glu Leu Asn
 145 150 155 160
 Ile Thr Ser Ala Thr Tyr Gln Ser Ala Ile Pro Pro Arg Gly Thr Gln
 165 170 175
 Ala Val Val Leu Xaa Val Tyr His Asn Ala Gly Gly Thr His Pro Thr
 180 185 190
 Thr Thr Tyr Lys Ala Phe Asp Trp Asp Gln Ala Tyr Arg Lys Pro Ile
 195 200 205
 Thr Tyr Asp Thr Leu Trp Gln Ala Asp Thr Asp Pro Leu Pro Val Val
 210 215 220
 Phe Pro Ile Val Ala Arg
 225 230

(2) INFORMATION FOR SEQ ID NO:66:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 132 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

Thr Ala Ala Ser Asp Asn Phe Gln Leu Ser Gln Gly Gly Gln Gly Phe
 1 5 10 15
 Ala Ile Pro Ile Gly Gln Ala Met Ala Ile Ala Gly Gln Ile Arg Ser
 20 25 30
 Gly Gly Gly Ser Pro Thr Val His Ile Gly Pro Thr Ala Phe Leu Gly
 35 40 45

98

Leu Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val Gln Arg Val
 50 55 60
 Val Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr Gly Asp Val
 65 70 75 80
 Ile Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr Ala Met Ala
 85 90 95
 Asp Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser Val Asn Trp
 100 105 110
 Gln Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr Leu Ala Glu
 115 120 125
 Gly Pro Pro Ala
 130

(2) INFORMATION FOR SEQ ID NO:67:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 100 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

Val Pro Leu Arg Ser Pro Ser Met Ser Pro Ser Lys Cys Leu Ala Ala
 1 5 10 15
 Ala Gln Arg Asn Pro Val Ile Arg Arg Arg Arg Leu Ser Asn Pro Pro
 20 25 30
 Pro Arg Lys Tyr Arg Ser Met Pro Ser Pro Ala Thr Ala Ser Ala Gly
 35 40 45
 Met Ala Arg Val Arg Arg Arg Ala Ile Trp Arg Gly Pro Ala Thr Xaa
 50 55 60
 Ser Ala Gly Met Ala Arg Val Arg Arg Trp Xaa Val Met Pro Xaa Val
 65 70 75 80
 Ile Gln Ser Thr Xaa Ile Arg Xaa Xaa Gly Pro Phe Asp Asn Arg Gly
 85 90 95
 Ser Glu Arg Lys
 100

(2) INFORMATION FOR SEQ ID NO:68:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 163 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

```

Met Thr Asp Asp Ile Leu Leu Ile Asp Thr Asp Glu Arg Val Arg Thr
1           5           10           15
Leu Thr Leu Asn Arg Pro Gln Ser Arg Asn Ala Leu Ser Ala Ala Leu
20           25           30
Arg Asp Arg Phe Phe Ala Xaa Leu Xaa Asp Ala Glu Xaa Asp Asp Asp
35           40           45
Ile Asp Val Val Ile Leu Thr Gly Ala Asp Pro Val Phe Cys Ala Gly
50           55           60
Leu Asp Leu Lys Val Ala Gly Arg Ala Asp Arg Ala Ala Gly His Leu
65           70           75           80
Thr Ala Val Gly Gly His Asp Gln Ala Gly Asp Arg Arg Asp Gln Arg
85           90           95
Arg Arg Gly His Arg Arg Ala Arg Thr Gly Ala Val Leu Arg His Pro
100          105          110
Asp Arg Leu Arg Ala Arg Pro Leu Arg Arg His Pro Arg Pro Gly Gly
115          120          125
Ala Ala Ala His Leu Gly Thr Gln Cys Val Leu Ala Ala Lys Gly Arg
130          135          140
His Arg Xaa Gly Pro Val Asp Glu Pro Asp Arg Arg Leu Pro Val Arg
145          150          155          160
Asp Arg Arg

```

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 344 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

```

Met Lys Phe Val Asn His Ile Glu Pro Val Ala Pro Arg Arg Ala Gly
1           5           10           15
Gly Ala Val Ala Glu Val Tyr Ala Glu Ala Arg Arg Glu Phe Gly Arg
20           25           30
Leu Pro Glu Pro Leu Ala Met Leu Ser Pro Asp Glu Gly Leu Leu Thr
35           40           45

```

100

Ala Gly Trp Ala Thr Leu Arg Glu Thr Leu Leu Val Gly Gln Val Pro
 50 55 60
 Arg Gly Arg Lys Glu Ala Val Ala Ala Ala Val Ala Ala Ser Leu Arg
 65 70 75 80
 Cys Pro Trp Cys Val Asp Ala His Thr Thr Met Leu Tyr Ala Ala Gly
 85 90 95
 Gln Thr Asp Thr Ala Ala Ala Ile Leu Ala Gly Thr Ala Pro Ala Ala
 100 105 110
 Gly Asp Pro Asn Ala Pro Tyr Val Ala Trp Ala Ala Gly Thr Gly Thr
 115 120 125
 Pro Ala Gly Pro Pro Ala Pro Phe Gly Pro Asp Val Ala Ala Glu Tyr
 130 135 140
 Leu Gly Thr Ala Val Gln Phe His Phe Ile Ala Arg Leu Val Leu Val
 145 150 155 160
 Leu Leu Asp Glu Thr Phe Leu Pro Gly Gly Pro Arg Ala Gln Gln Leu
 165 170 175
 Met Arg Arg Ala Gly Gly Leu Val Phe Ala Arg Lys Val Arg Ala Glu
 180 185 190
 His Arg Pro Gly Arg Ser Thr Arg Arg Leu Glu Pro Arg Thr Leu Pro
 195 200 205
 Asp Asp Leu Ala Trp Ala Thr Pro Ser Glu Pro Ile Ala Thr Ala Phe
 210 215 220
 Ala Ala Leu Ser His His Leu Asp Thr Ala Pro His Leu Pro Pro Pro
 225 230 235 240
 Thr Arg Gln Val Val Arg Arg Val Val Gly Ser Trp His Gly Glu Pro
 245 250 255
 Met Pro Met Ser Ser Arg Trp Thr Asn Glu His Thr Ala Glu Leu Pro
 260 265 270
 Ala Asp Leu His Ala Pro Thr Arg Leu Ala Leu Leu Thr Gly Leu Ala
 275 280 285
 Pro His Gln Val Thr Asp Asp Asp Val Ala Ala Ala Arg Ser Leu Leu
 290 295 300
 Asp Thr Asp Ala Ala Leu Val Gly Ala Leu Ala Trp Ala Ala Phe Thr
 305 310 315 320
 Ala Ala Arg Arg Ile Gly Thr Trp Ile Gly Ala Ala Ala Glu Gly Gln
 325 330 335
 Val Ser Arg Gln Asn Pro Thr Gly
 340

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 485 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

Asp	Asp	Pro	Asp	Met	Pro	Gly	Thr	Val	Ala	Lys	Ala	Val	Ala	Asp	Ala	1	5	10	15
Leu	Gly	Arg	Gly	Ile	Ala	Pro	Val	Glu	Asp	Ile	Gln	Asp	Cys	Val	Glu	20	25	30	
Ala	Arg	Leu	Gly	Glu	Ala	Gly	Leu	Asp	Asp	Val	Ala	Arg	Val	Tyr	Ile	35	40	45	
Ile	Tyr	Arg	Gln	Arg	Arg	Ala	Glu	Leu	Arg	Thr	Ala	Lys	Ala	Leu	Leu	50	55	60	
Gly	Val	Arg	Asp	Glu	Leu	Lys	Leu	Ser	Leu	Ala	Ala	Val	Thr	Val	Leu	65	70	75	80
Arg	Glu	Arg	Tyr	Leu	Leu	His	Asp	Glu	Gln	Gly	Arg	Pro	Ala	Glu	Ser	85	90	95	
Thr	Gly	Glu	Leu	Met	Asp	Arg	Ser	Ala	Arg	Cys	Val	Ala	Ala	Ala	Glu	100	105	110	
Asp	Gln	Tyr	Glu	Pro	Gly	Ser	Ser	Arg	Arg	Trp	Ala	Glu	Arg	Phe	Ala	115	120	125	
Thr	Leu	Leu	Arg	Asn	Leu	Glu	Phe	Leu	Pro	Asn	Ser	Pro	Thr	Leu	Met	130	135	140	
Asn	Ser	Gly	Thr	Asp	Leu	Gly	Leu	Leu	Ala	Gly	Cys	Phe	Val	Leu	Pro	145	150	155	160
Ile	Glu	Asp	Ser	Leu	Gln	Ser	Ile	Phe	Ala	Thr	Leu	Gly	Gln	Ala	Ala	165	170	175	
Glu	Leu	Gln	Arg	Ala	Gly	Gly	Gly	Thr	Gly	Tyr	Ala	Phe	Ser	His	Leu	180	185	190	
Arg	Pro	Ala	Gly	Asp	Arg	Val	Ala	Ser	Thr	Gly	Gly	Thr	Ala	Ser	Gly	195	200	205	
Pro	Val	Ser	Phe	Leu	Arg	Leu	Tyr	Asp	Ser	Ala	Ala	Gly	Val	Val	Ser	210	215	220	
Met	Gly	Gly	Arg	Arg	Arg	Gly	Ala	Cys	Met	Ala	Val	Leu	Asp	Val	Ser	225	230	235	240
His	Pro	Asp	Ile	Cys	Asp	Phe	Val	Thr	Ala	Lys	Ala	Glu	Ser	Pro	Ser	245	250	255	
Glu	Leu	Pro	His	Phe	Asn	Leu	Ser	Val	Gly	Val	Thr	Asp	Ala	Phe	Leu	260	265	270	
Arg	Ala	Val	Glu	Arg	Asn	Gly	Leu	His	Arg	Leu	Val	Asn	Pro	Arg	Thr	275	280	285	

102

Gly Lys Ile Val Ala Arg Met Pro Ala Ala Glu Leu Phe Asp Ala Ile
 290 295 300
 Cys Lys Ala Ala His Ala Gly Gly Asp Pro Gly Leu Val Phe Leu Asp
 305 310 315 320
 Thr Ile Asn Arg Ala Asn Pro Val Pro Gly Arg Gly Arg Ile Glu Ala
 325 330 335
 Thr Asn Pro Cys Gly Glu Val Pro Leu Leu Pro Tyr Glu Ser Cys Asn
 340 345 350
 Leu Gly Ser Ile Asn Leu Ala Arg Met Leu Ala Asp Gly Arg Val Asp
 355 360 365
 Trp Asp Arg Leu Glu Glu Val Ala Gly Val Ala Val Arg Phe Leu Asp
 370 375 380
 Asp Val Ile Asp Val Ser Arg Tyr Pro Phe Pro Glu Leu Gly Glu Ala
 385 390 395 400
 Ala Arg Ala Thr Arg Lys Ile Gly Leu Gly Val Met Gly Leu Ala Glu
 405 410 415
 Leu Leu Ala Ala Leu Gly Ile Pro Tyr Asp Ser Glu Glu Ala Val Arg
 420 425 430
 Leu Ala Thr Arg Leu Met Arg Arg Ile Gln Gln Ala Ala His Thr Ala
 435 440 445
 Ser Arg Arg Leu Ala Glu Glu Arg Gly Ala Phe Pro Ala Phe Thr Asp
 450 455 460
 Ser Arg Phe Ala Arg Ser Gly Pro Arg Arg Asn Ala Gln Val Thr Ser
 465 470 475 480
 Val Ala Pro Thr Gly
 485

(2) INFORMATION FOR SEQ ID NO:71:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 267 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

Gly Val Ile Val Leu Asp Leu Glu Pro Arg Gly Pro Leu Pro Thr Glu
 1 5 10 15
 Ile Tyr Trp Arg Arg Arg Gly Leu Ala Leu Gly Ile Ala Val Val Val
 20 25 30
 Val Gly Ile Ala Val Ala Ile Val Ile Ala Phe Val Asp Ser Ser Ala
 35 40 45

103

Gly Ala Lys Pro Val Ser Ala Asp Lys Pro Ala Ser Ala Gln Ser His
 50 55 60
 Pro Gly Ser Pro Ala Pro Gln Ala Pro Gln Pro Ala Gly Gln Thr Glu
 65 70 75 80
 Gly Asn Ala Ala Ala Pro Pro Gln Gly Gln Asn Pro Glu Thr Pro
 85 90 95
 Thr Pro Thr Ala Ala Val Gln Pro Pro Pro Val Leu Lys Glu Gly Asp
 100 105 110
 Asp Cys Pro Asp Ser Thr Leu Ala Val Lys Gly Leu Thr Asn Ala Pro
 115 120 125
 Gln Tyr Tyr Val Gly Asp Gln Pro Lys Phe Thr Met Val Val Thr Asn
 130 135 140
 Ile Gly Leu Val Ser Cys Lys Arg Asp Val Gly Ala Ala Val Leu Ala
 145 150 155 160
 Ala Tyr Val Tyr Ser Leu Asp Asn Lys Arg Leu Trp Ser Asn Leu Asp
 165 170 175
 Cys Ala Pro Ser Asn Glu Thr Leu Val Lys Thr Phe Ser Pro Gly Glu
 180 185 190
 Gln Val Thr Thr Ala Val Thr Trp Thr Gly Met Gly Ser Ala Pro Arg
 195 200 205
 Cys Pro Leu Pro Arg Pro Ala Ile Gly Pro Gly Thr Tyr Asn Leu Val
 210 215 220
 Val Gln Leu Gly Asn Leu Arg Ser Leu Pro Val Pro Phe Ile Leu Asn
 225 230 235 240
 Gln Pro Pro Pro Pro Pro Gly Pro Val Pro Ala Pro Gly Pro Ala Gln
 245 250 255
 Ala Pro Pro Pro Glu Ser Pro Ala Gln Gly Gly
 260 265

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

Leu Ile Ser Thr Gly Lys Ala Ser His Ala Ser Leu Gly Val Gln Val
 1 5 10 15
 Thr Asn Asp Lys Asp Thr Pro Gly Ala Lys Ile Val Glu Val Val Ala
 20 25 30

[illegible]

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 364 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

Gly 1	Ala	Ala	Val	Ser 5	Leu	Leu	Ala	Ala	Gly 10	Thr	Leu	Val	Leu	Thr 15	Ala
Cys	Gly	Gly	Gly 20	Thr	Asn	Ser	Ser	Ser 25	Ser	Gly	Ala	Gly	Gly 30	Thr	Ser
Gly	Ser	Val 35	His	Cys	Gly	Gly	Lys 40	Lys	Glu	Leu	His	Ser 45	Ser	Gly	Ser
Thr	Ala 50	Gln	Glu	Asn	Ala	Met 55	Glu	Gln	Phe	Val	Tyr 60	Ala	Tyr	Val	Arg
Ser 65	Cys	Pro	Gly	Tyr	Thr 70	Leu	Asp	Tyr	Asn	Ala 75	Asn	Gly	Ser	Gly	Ala 80
Gly	Val	Thr	Gln	Phe 85	Leu	Asn	Asn	Glu	Thr 90	Asp	Phe	Ala	Gly	Ser 95	Asp
Val	Pro	Leu	Asn 100	Pro	Ser	Thr	Gly	Gln 105	Pro	Asp	Arg	Ser	Ala 110	Glu	Arg
Cys	Gly	Ser 115	Pro	Ala	Trp	Asp	Leu 120	Pro	Thr	Val	Phe	Gly 125	Pro	Ile	Ala
Ile	Thr 130	Tyr	Asn	Ile	Lys	Gly 135	Val	Ser	Thr	Leu 140	Asn	Leu	Asp	Gly	Pro
Thr 145	Thr	Ala	Lys	Ile	Phe 150	Asn	Gly	Thr	Ile	Thr 155	Val	Trp	Asn	Asp	Pro 160
Gln	Ile	Gln	Ala	Leu 165	Asn	Ser	Gly	Thr	Asp 170	Leu	Pro	Pro	Thr	Pro 175	Ile

105

Ser Val Ile Phe Arg Ser Asp Lys Ser Gly Thr Ser Asp Asn Phe Gln
 180 185 190
 Lys Tyr Leu Asp Gly Val Ser Asn Gly Ala Trp Gly Lys Gly Ala Ser
 195 200 205
 Glu Thr Phe Ser Gly Gly Val Gly Val Gly Ala Ser Gly Asn Asn Gly
 210 215 220
 Thr Ser Ala Leu Leu Gln Thr Thr Asp Gly Ser Ile Thr Tyr Asn Glu
 225 230 235 240
 Trp Ser Phe Ala Val Gly Lys Gln Leu Asn Met Ala Gln Ile Ile Thr
 245 250 255
 Ser Ala Gly Pro Asp Pro Val Ala Ile Thr Thr Glu Ser Val Gly Lys
 260 265 270
 Thr Ile Ala Gly Ala Lys Ile Met Gly Gln Gly Asn Asp Leu Val Leu
 275 280 285
 Asp Thr Ser Ser Phe Tyr Arg Pro Thr Gln Pro Gly Ser Tyr Pro Ile
 290 295 300
 Val Leu Ala Thr Tyr Glu Ile Val Cys Ser Lys Tyr Pro Asp Ala Thr
 305 310 315 320
 Thr Gly Thr Ala Val Arg Ala Phe Met Gln Ala Ala Ile Gly Pro Gly
 325 330 335
 Gln Glu Gly Leu Asp Gln Tyr Gly Ser Ile Pro Leu Pro Lys Ser Phe
 340 345 350
 Gln Ala Lys Leu Ala Ala Ala Val Asn Ala Ile Ser
 355 360

(2) INFORMATION FOR SEQ ID NO:74:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 309 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

Gln Ala Ala Ala Gly Arg Ala Val Arg Arg Thr Gly His Ala Glu Asp
 1 5 10 15
 Gln Thr His Gln Asp Arg Leu His His Gly Cys Arg Arg Ala Ala Val
 20 25 30
 Val Val Arg Gln Asp Arg Ala Ser Val Ser Ala Thr Ser Ala Arg Pro
 35 40 45
 Pro Arg Arg His Pro Ala Gln Gly His Arg Arg Arg Val Ala Pro Ser
 50 55 60

Gly Gly Arg Arg Arg Pro His Pro His His Val Gln Pro Asp Asp Arg
 65 70 75 80
 Arg Asp Arg Pro Ala Leu Leu Asp Arg Thr Gln Pro Ala Glu His Pro
 85 90 95
 Asp Pro His Arg Arg Gly Pro Ala Asp Pro Gly Arg Val Arg Gly Arg
 100 105 110
 Gly Arg Leu Arg Arg Val Asp Asp Gly Arg Leu Gln Pro Asp Arg Asp
 115 120 125
 Ala Asp His Gly Ala Pro Val Arg Gly Arg Gly Pro His Arg Gly Val
 130 135 140
 Gln His Arg Gly Gly Pro Val Phe Val Arg Arg Val Pro Gly Val Arg
 145 150 155 160
 Cys Ala His Arg Arg Gly His Arg Arg Val Ala Ala Pro Gly Gln Gly
 165 170 175
 Asp Val Leu Arg Ala Gly Leu Arg Val Glu Arg Leu Arg Pro Val Ala
 180 185 190
 Ala Val Glu Asn Leu His Arg Gly Ser Gln Arg Ala Asp Gly Arg Val
 195 200 205
 Phe Arg Pro Ile Arg Arg Gly Ala Arg Leu Pro Ala Arg Arg Ser Arg
 210 215 220
 Ala Gly Pro Gln Gly Arg Leu His Leu Asp Gly Ala Gly Pro Ser Pro
 225 230 235 240
 Leu Pro Ala Arg Ala Gly Gln Gln Gln Pro Ser Ser Ala Gly Gly Arg
 245 250 255
 Arg Ala Gly Gly Ala Glu Arg Ala Asp Pro Gly Gln Arg Gly Arg His
 260 265 270
 His Gln Gly Gly His Asp Pro Gly Arg Gln Gly Ala Gln Arg Gly Thr
 275 280 285
 Ala Gly Val Ala His Ala Ala Ala Gly Pro Arg Arg Ala Ala Val Arg
 290 295 300
 Asn Arg Pro Arg Arg
 305

(2) INFORMATION FOR SEQ ID NO:75:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 580 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

107

Ser Ala Val Trp Cys Leu Asn Gly Phe Thr Gly Arg His Arg His Gly
 1 5 10 15
 Arg Cys Arg Val Arg Ala Ser Gly Trp Arg Ser Ser Asn Arg Trp Cys
 20 25 30
 Ser Thr Thr Ala Asp Cys Cys Ala Ser Lys Thr Pro Thr Gln Ala Ala
 35 40 45
 Ser Pro Leu Glu Arg Arg Phe Thr Cys Cys Ser Pro Ala Val Gly Cys
 50 55 60
 Arg Phe Arg Ser Phe Pro Val Arg Arg Leu Ala Leu Gly Ala Arg Thr
 65 70 75 80
 Ser Arg Thr Leu Gly Val Arg Arg Thr Leu Ser Gln Trp Asn Leu Ser
 85 90 95
 Pro Arg Ala Gln Pro Ser Cys Ala Val Thr Val Glu Ser His Thr His
 100 105 110
 Ala Ser Pro Arg Met Ala Lys Leu Ala Arg Val Val Gly Leu Val Gln
 115 120 125
 Glu Glu Gln Pro Ser Asp Met Thr Asn His Pro Arg Tyr Ser Pro Pro
 130 135 140
 Pro Gln Gln Pro Gly Thr Pro Gly Tyr Ala Gln Gly Gln Gln Gln Thr
 145 150 155 160
 Tyr Ser Gln Gln Phe Asp Trp Arg Tyr Pro Pro Ser Pro Pro Pro Gln
 165 170 175
 Pro Thr Gln Tyr Arg Gln Pro Tyr Glu Ala Leu Gly Gly Thr Arg Pro
 180 185 190
 Gly Leu Ile Pro Gly Val Ile Pro Thr Met Thr Pro Pro Gly Met
 195 200 205
 Val Arg Gln Arg Pro Arg Ala Gly Met Leu Ala Ile Gly Ala Val Thr
 210 215 220
 Ile Ala Val Val Ser Ala Gly Ile Gly Gly Ala Ala Ala Ser Leu Val
 225 230 235 240
 Gly Phe Asn Arg Ala Pro Ala Gly Pro Ser Gly Gly Pro Val Ala Ala
 245 250 255
 Ser Ala Ala Pro Ser Ile Pro Ala Ala Asn Met Pro Pro Gly Ser Val
 260 265 270
 Glu Gln Val Ala Ala Lys Val Val Pro Ser Val Val Met Leu Glu Thr
 275 280 285
 Asp Leu Gly Arg Gln Ser Glu Glu Gly Ser Gly Ile Ile Leu Ser Ala
 290 295 300
 Glu Gly Leu Ile Leu Thr Asn Asn His Val Ile Ala Ala Ala Ala Lys
 305 310 315 320
 Pro Pro Leu Gly Ser Pro Pro Pro Lys Thr Thr Val Thr Phe Ser Asp

[illegible]

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

```

Met Asn Asp Gly Lys Arg Ala Val Thr Ser Ala Val Leu Val Val Leu
1          5          10          15
Gly Ala Cys Leu Ala Leu Trp Leu Ser Gly Cys Ser Ser Pro Lys Pro
20          25          30
Asp Ala Glu Glu Gln Gly Val Pro Val Ser Pro Thr Ala Ser Asp Pro
35          40          45
Ala Leu Leu Ala Glu Ile Arg Gln Ser Leu Asp Ala Thr Lys Gly Leu
50          55          60
Thr Ser Val His Val Ala Val Arg Thr Thr Gly Lys Val Asp Ser Leu
65          70          75          80
Leu Gly Ile Thr Ser Ala Asp Val Asp Val Arg Ala Asn Pro Leu Ala
85          90          95
Ala Lys Gly Val Cys Thr Tyr Asn Asp Glu Gln Gly Val Pro Phe Arg
100         105         110
Val Gln Gly Asp Asn Ile Ser Val Lys Leu Phe Asp Asp Trp Ser Asn
115         120         125
Leu Gly Ser Ile Ser Glu Leu Ser Thr Ser Arg Val Leu Asp Pro Ala
130         135         140
Ala Gly Val Thr Gln Leu Leu Ser Gly Val Thr Asn Leu Gln Ala Gln
145         150         155         160
Gly Thr Glu Val Ile Asp Gly Ile Ser Thr Thr Lys Ile Thr Gly Thr
165         170         175
Ile Pro Ala Ser Ser Val Lys Met Leu Asp Pro Gly Ala Lys Ser Ala
180         185         190
Arg Pro Ala Thr Val Trp Ile Ala Gln Asp Gly Ser His His Leu Val
195         200         205
Arg Ala Ser Ile Asp Leu Gly Ser Gly Ser Ile Gln Leu Thr Gln Ser
210         215         220
Lys Trp Asn Glu Pro Val Asn Val Asp
225         230

```

(2) INFORMATION FOR SEQ ID NO:77:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 66 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

```

Val Ile Asp Ile Ile Gly Thr Ser Pro Thr Ser Trp Glu Gln Ala Ala

```

110

```

1             5             10             15
Ala Glu Ala Val Gln Arg Ala Arg Asp Ser Val Asp Asp Ile Arg Val
                20                25                30
Ala Arg Val Ile Glu Gln Asp Met Ala Val Asp Ser Ala Gly Lys Ile
                35                40                45
Thr Tyr Arg Ile Lys Leu Glu Val Ser Phe Lys Met Arg Pro Ala Gln
                50                55                60
Pro Arg
65

```

(2) INFORMATION FOR SEQ ID NO:78:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 69 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

```

Val Pro Pro Ala Pro Pro Leu Pro Pro Leu Pro Pro Ser Pro Ile Ser
1             5             10             15
Cys Ala Ser Pro Pro Ser Pro Pro Leu Pro Pro Ala Pro Pro Val Ala
                20                25                30
Pro Gly Pro Pro Met Pro Pro Leu Asp Pro Trp Pro Pro Ala Pro Pro
                35                40                45
Leu Pro Tyr Ser Thr Pro Pro Gly Ala Pro Leu Pro Pro Ser Pro Pro
                50                55                60
Ser Pro Pro Leu Pro
65

```

(2) INFORMATION FOR SEQ ID NO:79:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 355 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

```

Met Ser Asn Ser Arg Arg Arg Ser Leu Arg Trp Ser Trp Leu Leu Ser
1             5             10             15
Val Leu Ala Ala Val Gly Leu Gly Leu Ala Thr Ala Pro Ala Gln Ala
                20                25                30

```

[illegible]

355

(2) INFORMATION FOR SEQ ID NO:80:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 205 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

```

Ser Pro Lys Pro Asp Ala Glu Glu Gln Gly Val Pro Val Ser Pro Thr
1                               5               10               15

Ala Ser Asp Pro Ala Leu Leu Ala Glu Ile Arg Gln Ser Leu Asp Ala
                20               25               30

Thr Lys Gly Leu Thr Ser Val His Val Ala Val Arg Thr Thr Gly Lys
                35               40               45

Val Asp Ser Leu Leu Gly Ile Thr Ser Ala Asp Val Asp Val Arg Ala
                50               55               60

Asn Pro Leu Ala Ala Lys Gly Val Cys Thr Tyr Asn Asp Glu Gln Gly
65                70               75               80

Val Pro Phe Arg Val Gln Gly Asp Asn Ile Ser Val Lys Leu Phe Asp
                85               90               95

Asp Trp Ser Asn Leu Gly Ser Ile Ser Glu Leu Ser Thr Ser Arg Val
                100              105              110

Leu Asp Pro Ala Ala Gly Val Thr Gln Leu Leu Ser Gly Val Thr Asn
                115              120              125

Leu Gln Ala Gln Gly Thr Glu Val Ile Asp Gly Ile Ser Thr Thr Lys
                130              135              140

Ile Thr Gly Thr Ile Pro Ala Ser Ser Val Lys Met Leu Asp Pro Gly
145              150              155              160

Ala Lys Ser Ala Arg Pro Ala Thr Val Trp Ile Ala Gln Asp Gly Ser
                165              170              175

His His Leu Val Arg Ala Ser Ile Asp Leu Gly Ser Gly Ser Ile Gln
                180              185              190

Leu Thr Gln Ser Lys Trp Asn Glu Pro Val Asn Val Asp
                195              200              205

```

(2) INFORMATION FOR SEQ ID NO:81:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 286 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

Gly Asp Ser Phe Trp Ala Ala Ala Asp Gln Met Ala Arg Gly Phe Val
 1 5 10 15
 Leu Gly Ala Thr Ala Gly Arg Thr Thr Leu Thr Gly Glu Gly Leu Gln
 20 25 30
 His Ala Asp Gly His Ser Leu Leu Leu Asp Ala Thr Asn Pro Ala Val
 35 40 45
 Val Ala Tyr Asp Pro Ala Phe Ala Tyr Glu Ile Gly Tyr Ile Xaa Glu
 50 55 60
 Ser Gly Leu Ala Arg Met Cys Gly Glu Asn Pro Glu Asn Ile Phe Phe
 65 70 75 80
 Tyr Ile Thr Val Tyr Asn Glu Pro Tyr Val Gln Pro Pro Glu Pro Glu
 85 90 95
 Asn Phe Asp Pro Glu Gly Val Leu Gly Gly Ile Tyr Arg Tyr His Ala
 100 105 110
 Ala Thr Glu Gln Arg Thr Asn Lys Xaa Gln Ile Leu Ala Ser Gly Val
 115 120 125
 Ala Met Pro Ala Ala Leu Arg Ala Ala Gln Met Leu Ala Ala Glu Trp
 130 135 140
 Asp Val Ala Ala Asp Val Trp Ser Val Thr Ser Trp Gly Glu Leu Asn
 145 150 155 160
 Arg Asp Gly Val Val Ile Glu Thr Glu Lys Leu Arg His Pro Asp Arg
 165 170 175
 Pro Ala Gly Val Pro Tyr Val Thr Arg Ala Leu Glu Asn Ala Arg Gly
 180 185 190
 Pro Val Ile Ala Val Ser Asp Trp Met Arg Ala Val Pro Glu Gln Ile
 195 200 205
 Arg Pro Trp Val Pro Gly Thr Tyr Leu Thr Leu Gly Thr Asp Gly Phe
 210 215 220
 Gly Phe Ser Asp Thr Arg Pro Ala Gly Arg Arg Tyr Phe Asn Thr Asp
 225 230 235 240
 Ala Glu Ser Gln Val Gly Arg Gly Phe Gly Arg Gly Trp Pro Gly Arg
 245 250 255
 Arg Val Asn Ile Asp Pro Phe Gly Ala Gly Arg Gly Pro Pro Ala Gln
 260 265 270
 Leu Pro Gly Phe Asp Glu Gly Gly Gly Leu Arg Pro Xaa Lys
 275 280 285

(2) INFORMATION FOR SEQ ID NO:82:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 173 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

```

Thr Lys Phe His Ala Leu Met Gln Glu Gln Ile His Asn Glu Phe Thr
1          5          10          15
Ala Ala Gln Gln Tyr Val Ala Ile Ala Val Tyr Phe Asp Ser Glu Asp
20          25          30
Leu Pro Gln Leu Ala Lys His Phe Tyr Ser Gln Ala Val Glu Glu Arg
35          40          45
Asn His Ala Met Met Leu Val Gln His Leu Leu Asp Arg Asp Leu Arg
50          55          60
Val Glu Ile Pro Gly Val Asp Thr Val Arg Asn Gln Phe Asp Arg Pro
65          70          75          80
Arg Glu Ala Leu Ala Leu Ala Leu Asp Gln Glu Arg Thr Val Thr Asp
85          90          95
Gln Val Gly Arg Leu Thr Ala Val Ala Arg Asp Glu Gly Asp Phe Leu
100         105         110
Gly Glu Gln Phe Met Gln Trp Phe Leu Gln Glu Gln Ile Glu Glu Val
115         120         125
Ala Leu Met Ala Thr Leu Val Arg Val Ala Asp Arg Ala Gly Ala Asn
130         135         140
Leu Phe Glu Leu Glu Asn Phe Val Ala Arg Glu Val Asp Val Ala Pro
145         150         155         160
Ala Ala Ser Gly Ala Pro His Ala Ala Gly Gly Arg Leu
165         170

```

(2) INFORMATION FOR SEQ ID NO:83:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 107 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

```

Arg Ala Asp Glu Arg Lys Asn Thr Thr Met Lys Met Val Lys Ser Ile
1          5          10          15

```


115

Ala Ala Gly Leu Thr Ala Ala Ala Ala Ile Gly Ala Ala Ala Ala Gly
 20 25 30

Val Thr Ser Ile Met Ala Gly Gly Pro Val Val Tyr Gln Met Gln Pro
 35 40 45

Val Val Phe Gly Ala Pro Leu Pro Leu Asp Pro Xaa Ser Ala Pro Xaa
 50 55 60

Val Pro Thr Ala Ala Gln Trp Thr Xaa Leu Leu Asn Xaa Leu Xaa Asp
 65 70 75 80

Pro Asn Val Ser Phe Xaa Asn Lys Gly Ser Leu Val Glu Gly Gly Ile
 85 90 95

Gly Gly Xaa Glu Gly Xaa Xaa Arg Arg Xaa Gln
 100 105

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

Val Leu Ser Val Pro Val Gly Asp Gly Phe Trp Xaa Arg Val Val Asn
 1 5 10 15

Pro Leu Gly Gln Pro Ile Asp Gly Arg Gly Asp Val Asp Ser Asp Thr
 20 25 30

Arg Arg Ala Leu Glu Leu Gln Ala Pro Ser Val Val Xaa Arg Gln Gly
 35 40 45

Val Lys Glu Pro Leu Xaa Thr Gly Ile Lys Ala Ile Asp Ala Met Thr
 50 55 60

Pro Ile Gly Arg Gly Gln Arg Gln Leu Ile Ile Gly Asp Arg Lys Thr
 65 70 75 80

Gly Lys Asn Arg Arg Leu Cys Arg Thr Pro Ser Ser Asn Gln Arg Glu
 85 90 95

Glu Leu Gly Val Arg Trp Ile Pro Arg Ser Arg Cys Ala Cys Val Tyr
 100 105 110

Val Gly His Arg Ala Arg Arg Gly Thr Tyr His Arg Arg
 115 120 125

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

```

Cys Asp Ala Val Met Gly Phe Leu Gly Gly Ala Gly Pro Leu Ala Val
1           5           10           15
Val Asp Gln Gln Leu Val Thr Arg Val Pro Gln Gly Trp Ser Phe Ala
20           25           30
Gln Ala Ala Ala Val Pro Val Val Phe Leu Thr Ala Trp Tyr Gly Leu
35           40           45
Ala Asp Leu Ala Glu Ile Lys Ala Gly Glu Ser Val Leu Ile His Ala
50           55           60
Gly Thr Gly Gly Val Gly Met Ala Ala Val Gln Leu Ala Arg Gln Trp
65           70           75           80
Gly Val Glu Val Phe Val Thr Ala Ser Arg Gly Lys Trp Asp Thr Leu
85           90           95
Arg Ala Xaa Xaa Phe Asp Asp Xaa Pro Tyr Arg Xaa Phe Pro His Xaa
100          105          110
Arg Ser Ser Xaa Gly
115

```

(2) INFORMATION FOR SEQ ID NO:86:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 103 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

```

Met Tyr Arg Phe Ala Cys Arg Thr Leu Met Leu Ala Ala Cys Ile Leu
1           5           10           15
Ala Thr Gly Val Ala Gly Leu Gly Val Gly Ala Gln Ser Ala Ala Gln
20           25           30
Thr Ala Pro Val Pro Asp Tyr Tyr Trp Cys Pro Gly Gln Pro Phe Asp
35           40           45
Pro Ala Trp Gly Pro Asn Trp Asp Pro Tyr Thr Cys His Asp Asp Phe
50           55           60
His Arg Asp Ser Asp Gly Pro Asp His Ser Arg Asp Tyr Pro Gly Pro
65           70           75           80
Ile Leu Glu Gly Pro Val Leu Asp Asp Pro Gly Ala Ala Pro Pro Pro

```

117

85

90

95

Pro Ala Ala Gly Gly Gly Ala
100

(2) INFORMATION FOR SEQ ID NO:87:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 88 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

Val	Gln	Cys	Arg	Val	Trp	Leu	Glu	Ile	Gln	Trp	Arg	Gly	Met	Leu	Gly
1				5					10					15	
Ala	Asp	Gln	Ala	Arg	Ala	Gly	Gly	Pro	Ala	Arg	Ile	Trp	Arg	Glu	His
			20					25					30		
Ser	Met	Ala	Ala	Met	Lys	Pro	Arg	Thr	Gly	Asp	Gly	Pro	Leu	Glu	Ala
		35				40						45			
Thr	Lys	Glu	Gly	Arg	Gly	Ile	Val	Met	Arg	Val	Pro	Leu	Glu	Gly	Gly
	50					55					60				
Gly	Arg	Leu	Val	Val	Glu	Leu	Thr	Pro	Asp	Glu	Ala	Ala	Ala	Leu	Gly
65					70					75					80
Asp	Glu	Leu	Lys	Gly	Val	Thr	Ser								
					85										

(2) INFORMATION FOR SEQ ID NO:88:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 95 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

Thr	Asp	Ala	Ala	Thr	Leu	Ala	Gln	Glu	Ala	Gly	Asn	Phe	Glu	Arg	Ile
1				5					10					15	
Ser	Gly	Asp	Leu	Lys	Thr	Gln	Ile	Asp	Gln	Val	Glu	Ser	Thr	Ala	Gly
			20					25					30		
Ser	Leu	Gln	Gly	Gln	Trp	Arg	Gly	Ala	Ala	Gly	Thr	Ala	Ala	Gln	Ala
		35					40					45			
Ala	Val	Val	Arg	Phe	Gln	Glu	Ala	Ala	Asn	Lys	Gln	Lys	Gln	Glu	Leu
	50					55						60			

118

Asp Glu Ile Ser Thr Asn Ile Arg Gln Ala Gly Val Gln Tyr Ser Arg
 65 70 75 80

Ala Asp Glu Glu Gln Gln Gln Ala Leu Ser Ser Gln Met Gly Phe
 85 90 95

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 166 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

Met Thr Gln Ser Gln Thr Val Thr Val Asp Gln Gln Glu Ile Leu Asn
 1 5 10 15
 Arg Ala Asn Glu Val Glu Ala Pro Met Ala Asp Pro Pro Thr Asp Val
 20 25 30
 Pro Ile Thr Pro Cys Glu Leu Thr Xaa Xaa Lys Asn Ala Ala Gln Gln
 35 40 45
 Xaa Val Leu Ser Ala Asp Asn Met Arg Glu Tyr Leu Ala Ala Gly Ala
 50 55 60
 Lys Glu Arg Gln Arg Leu Ala Thr Ser Leu Arg Asn Ala Ala Lys Xaa
 65 70 75 80
 Tyr Gly Glu Val Asp Glu Glu Ala Ala Thr Ala Leu Asp Asn Asp Gly
 85 90 95
 Glu Gly Thr Val Gln Ala Glu Ser Ala Gly Ala Val Gly Gly Asp Ser
 100 105 110
 Ser Ala Glu Leu Thr Asp Thr Pro Arg Val Ala Thr Ala Gly Glu Pro
 115 120 125
 Asn Phe Met Asp Leu Lys Glu Ala Ala Arg Lys Leu Glu Thr Gly Asp
 130 135 140
 Gln Gly Ala Ser Leu Ala His Xaa Gly Asp Gly Trp Asn Thr Xaa Thr
 145 150 155 160
 Leu Thr Leu Gln Gly Asp
 165

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

Arg Ala Glu Arg Met
1 5

(2) INFORMATION FOR SEQ ID NO:91:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 263 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

Val	Ala	Trp	Met	Ser	Val	Thr	Ala	Gly	Gln	Ala	Glu	Leu	Thr	Ala	Ala	
1				5					10					15		
Gln	Val	Arg	Val	Ala	Ala	Ala	Ala	Tyr	Glu	Thr	Ala	Tyr	Gly	Leu	Thr	
			20					25					30			
Val	Pro	Pro	Pro	Val	Ile	Ala	Glu	Asn	Arg	Ala	Glu	Leu	Met	Ile	Leu	
			35				40					45				
Ile	Ala	Thr	Asn	Leu	Leu	Gly	Gln	Asn	Thr	Pro	Ala	Ile	Ala	Val	Asn	
	50					55					60					
Glu	Ala	Glu	Tyr	Gly	Glu	Met	Trp	Ala	Gln	Asp	Ala	Ala	Ala	Met	Phe	
65					70				75						80	
Gly	Tyr	Ala	Ala	Ala	Thr	Ala	Thr	Ala	Thr	Ala	Thr	Leu	Leu	Pro	Phe	
				85					90					95		
Glu	Glu	Ala	Pro	Glu	Met	Thr	Ser	Ala	Gly	Gly	Leu	Leu	Glu	Gln	Ala	
			100					105					110			
Ala	Ala	Val	Glu	Glu	Ala	Ser	Asp	Thr	Ala	Ala	Ala	Asn	Gln	Leu	Met	
		115					120					125				
Asn	Asn	Val	Pro	Gln	Ala	Leu	Lys	Gln	Leu	Ala	Gln	Pro	Thr	Gln	Gly	
	130					135					140					
Thr	Thr	Pro	Ser	Ser	Lys	Leu	Gly	Gly	Leu	Trp	Lys	Thr	Val	Ser	Pro	
145					150					155					160	
His	Arg	Ser	Pro	Ile	Ser	Asn	Met	Val	Ser	Met	Ala	Asn	Asn	His	Met	
				165					170					175		
Ser	Met	Thr	Asn	Ser	Gly	Val	Ser	Met	Thr	Asn	Thr	Leu	Ser	Ser	Met	
			180					185					190			
Leu	Lys	Gly	Phe	Ala	Pro	Ala	Ala	Ala	Gln	Ala	Val	Gln	Thr	Ala		
		195					200				205					

120

Ala Gln Asn Gly Val Arg Ala Met Ser Ser Leu Gly Ser Ser Leu Gly
 210 215 220

Ser Ser Gly Leu Gly Gly Gly Val Ala Ala Asn Leu Gly Arg Ala Ala
 225 230 235 240

Ser Val Arg Tyr Gly His Arg Asp Gly Gly Lys Tyr Ala Xaa Ser Gly
 245 250 255

Arg Arg Asn Gly Gly Pro Ala
 260

(2) INFORMATION FOR SEQ ID NO:92:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 303 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

Met Thr Tyr Ser Pro Gly Asn Pro Gly Tyr Pro Gln Ala Gln Pro Ala
 1 5 10 15

Gly Ser Tyr Gly Gly Val Thr Pro Ser Phe Ala His Ala Asp Glu Gly
 20 25 30

Ala Ser Lys Leu Pro Met Tyr Leu Asn Ile Ala Val Ala Val Leu Gly
 35 40 45

Leu Ala Ala Tyr Phe Ala Ser Phe Gly Pro Met Phe Thr Leu Ser Thr
 50 55 60

Glu Leu Gly Gly Gly Asp Gly Ala Val Ser Gly Asp Thr Gly Leu Pro
 65 70 75 80

Val Gly Val Ala Leu Leu Ala Ala Leu Leu Ala Gly Val Val Leu Val
 85 90 95

Pro Lys Ala Lys Ser His Val Thr Val Val Ala Val Leu Gly Val Leu
 100 105 110

Gly Val Phe Leu Met Val Ser Ala Thr Phe Asn Lys Pro Ser Ala Tyr
 115 120 125

Ser Thr Gly Trp Ala Leu Trp Val Val Leu Ala Phe Ile Val Phe Gln
 130 135 140

Ala Val Ala Ala Val Leu Ala Leu Leu Val Glu Thr Gly Ala Ile Thr
 145 150 155 160

Ala Pro Ala Pro Arg Pro Lys Phe Asp Pro Tyr Gly Gln Tyr Gly Arg
 165 170 175

Tyr Gly Gln Tyr Gly Gln Tyr Gly Val Gln Pro Gly Gly Tyr Tyr Gly
 180 185 190

121

Gln Gln Gly Ala Gln Gln Ala Ala Gly Leu Gln Ser Pro Gly Pro Gln
 195 200 205

Gln Ser Pro Gln Pro Pro Gly Tyr Gly Ser Gln Tyr Gly Gly Tyr Ser
 210 215 220

Ser Ser Pro Ser Gln Ser Gly Ser Gly Tyr Thr Ala Gln Pro Pro Ala
 225 230 235 240

Gln Pro Pro Ala Gln Ser Gly Ser Gln Gln Ser His Gln Gly Pro Ser
 245 250 255

Thr Pro Pro Thr Gly Phe Pro Ser Phe Ser Pro Pro Pro Pro Val Ser
 260 265 270

Ala Gly Thr Gly Ser Gln Ala Gly Ser Ala Pro Val Asn Tyr Ser Asn
 275 280 285

Pro Ser Gly Gly Glu Gln Ser Ser Ser Pro Gly Gly Ala Pro Val
 290 295 300

(2) INFORMATION FOR SEQ ID NO:93:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 28 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

Gly Cys Gly Glu Thr Asp Ala Ala Thr Leu Ala Gln Glu Ala Gly Asn
 1 5 10 15

Phe Glu Arg Ile Ser Gly Asp Leu Lys Thr Gln Ile
 20 25

(2) INFORMATION FOR SEQ ID NO:94:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 16 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

Asp Gln Val Glu Ser Thr Ala Gly Ser Leu Gln Gly Gln Trp Arg Gly
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:95:

- (i) SEQUENCE CHARACTERISTICS:

122

- (A) LENGTH: 27 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

```

Gly Cys Gly Ser Thr Ala Gly Ser Leu Gln Gly Gln Trp Arg Gly Ala
1           5           10           15
Ala Gly Thr Ala Ala Gln Ala Ala Val Val Arg
          20           25

```

(2) INFORMATION FOR SEQ ID NO:96:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

```

Gly Cys Gly Gly Thr Ala Ala Gln Ala Ala Val Val Arg Phe Gln Glu
1           5           10           15
Ala Ala Asn Lys Gln Lys Gln Glu Leu Asp Glu
          20           25

```

(2) INFORMATION FOR SEQ ID NO:97:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

```

Gly Cys Gly Ala Asn Lys Gln Lys Gln Glu Leu Asp Glu Ile Ser Thr
1           5           10           15
Asn Ile Arg Gln Ala Gly Val Gln Tyr Ser Arg
          20           25

```

(2) INFORMATION FOR SEQ ID NO:98:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 amino acids
 - (B) TYPE: amino acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

Gly	Cys	Gly	Ile	Arg	Gln	Ala	Gly	Val	Gln	Tyr	Ser	Arg	Ala	Asp	Glu
1				5				10						15	
Glu	Gln	Gln	Gln	Ala	Leu	Ser	Ser	Gln	Met	Gly	Phe				
			20					25							

(2) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 507 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

ATGAAGATGG	TGAAATCGAT	CGCCGCAGGT	CTGACCGCCG	CGGCTGCAAT	CGGCGCCGCT	60
GCGGCCGGTG	TGACTTCGAT	CATGGCTGGC	GGCCCGGTCTG	TATACCAGAT	GCAGCCGGTC	120
GTCTTCGGCG	CGCCACTGCC	GTTGGACCCG	GCATCCGCCC	CTGACGTCCC	GACCGCCGCC	180
CAGTTGACCA	GCCTGCTCAA	CAGCCTCGCC	GATCCCAACG	TGTCGTTTGC	GAACAAGGGC	240
AGTCTGGTCG	AGGGCGGCAT	CGGGGGCACC	GAGGCGCGCA	TCGCCGACCA	CAAGCTGAAG	300
AAGGCCGCCG	AGCACGGGGA	TCTGCCGCTG	TCGTTACGCG	TGACGAACAT	CCAGCCGGCG	360
GCCGCCGGTT	CGGCCACCGC	CGACGTTTCC	GTCTCGGGTC	CGAAGCTCTC	GTCGCCGGTC	420
ACGCAGAACG	TCACGTTTCG	GAATCAAGGC	GGCTGGATGC	TGTCACGCGC	ATCGGCGATG	480
GAGTTGCTGC	AGGCCGCAGG	GAAGTGA				507

(2) INFORMATION FOR SEQ ID NO:100:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 168 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

124

Met Lys Met Val Lys Ser Ile Ala Ala Gly Leu Thr Ala Ala Ala Ala
 1 5 10 15
 Ile Gly Ala Ala Ala Ala Gly Val Thr Ser Ile Met Ala Gly Gly Pro
 20 25 30
 Val Val Tyr Gln Met Gln Pro Val Val Phe Gly Ala Pro Leu Pro Leu
 35 40 45
 Asp Pro Ala Ser Ala Pro Asp Val Pro Thr Ala Ala Gln Leu Thr Ser
 50 55 60
 Leu Leu Asn Ser Leu Ala Asp Pro Asn Val Ser Phe Ala Asn Lys Gly
 65 70 75 80
 Ser Leu Val Glu Gly Gly Ile Gly Gly Thr Glu Ala Arg Ile Ala Asp
 85 90 95
 His Lys Leu Lys Lys Ala Ala Glu His Gly Asp Leu Pro Leu Ser Phe
 100 105 110
 Ser Val Thr Asn Ile Gln Pro Ala Ala Ala Gly Ser Ala Thr Ala Asp
 115 120 125
 Val Ser Val Ser Gly Pro Lys Leu Ser Ser Pro Val Thr Gln Asn Val
 130 135 140
 Thr Phe Val Asn Gln Gly Gly Trp Met Leu Ser Arg Ala Ser Ala Met
 145 150 155 160
 Glu Leu Leu Gln Ala Ala Gly Asn
 165

(2) INFORMATION FOR SEQ ID NO:101:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 500 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

CGTGGCAATG TCGTTGACCG TCGGGGCCCG GTTCGCCTCC GCAGATCCCG TGGACGCGGT 60
 CATTAACACC ACCTGCAATT ACGGGCAGGT AGTAGCTGCG CTCAACGCGA CGGATCCGGG 120
 GGCTGCCGCA CAGTTCAACG CCTCACCAGT GGCGCAGTCC TATTTGCGCA ATTCCTCGC 180
 CGCACCGCCA CCTCAGCGCG CTGCCATGGC CGCGCAATTG CAAGCTGTGC CGGGGGCGGC 240
 ACAGTACATC GGCCTTGTGC AGTCGGTTGC CGGCTCCTGC AACAACTATT AAGCCCATGC 300
 GGGCCCCATC CCGCGACCCG GCATCGTCGC CGGGGCTAGG CCAGATTGCC CCGCTCCTCA 360
 ACGGGCCGCA TCCCGCGACC CGGCATCGTC GCCGGGGCTA GGCCAGATTG CCGCTCCTCA 420
 CAACGGGCCG CATCTCGTGC CGAATTCCTG CAGCCCGGGG GATCCACTAG TTCTAGAGCG 480

GCCGCCACCG CGGTGGAGCT

500

(2) INFORMATION FOR SEQ ID NO:102:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 96 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

```

Val Ala Met Ser Leu Thr Val Gly Ala Gly Val Ala Ser Ala Asp Pro
1           5           10           15
Val Asp Ala Val Ile Asn Thr Thr Cys Asn Tyr Gly Gln Val Val Ala
20          25          30
Ala Leu Asn Ala Thr Asp Pro Gly Ala Ala Ala Gln Phe Asn Ala Ser
35          40          45
Pro Val Ala Gln Ser Tyr Leu Arg Asn Phe Leu Ala Ala Pro Pro Pro
50          55          60
Gln Arg Ala Ala Met Ala Ala Gln Leu Gln Ala Val Pro Gly Ala Ala
65          70          75          80
Gln Tyr Ile Gly Leu Val Glu Ser Val Ala Gly Ser Cys Asn Asn Tyr
85          90          95

```

(2) INFORMATION FOR SEQ ID NO:103:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 154 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

```

ATGACAGAGC AGCAGTGGAA TTTCGCGGGT ATCGAGGCCG CGGCAAGCGC AATCCAGGGA      60
AATGTCACGT CCATTCATTC CCTCCTTGAC GAGGGGAAGC AGTCCCTGAC CAAGCTCGCA      120
GCGGCCTGGG GCGGTAGCGG TTCGGAAGCG TACC                                154

```

(2) INFORMATION FOR SEQ ID NO:104:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 51 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

```

Met Thr Glu Gln Gln Trp Asn Phe Ala Gly Ile Glu Ala Ala Ala Ser
1           5           10           15

Ala Ile Gln Gly Asn Val Thr Ser Ile His Ser Leu Leu Asp Glu Gly
          20           25           30

Lys Gln Ser Leu Thr Lys Leu Ala Ala Ala Trp Gly Gly Ser Gly Ser
          35           40           45

Glu Ala Tyr
          50

```

(2) INFORMATION FOR SEQ ID NO:105:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 282 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

```

CGGTCGCGCA CTTCCAGGTG ACTATGAAAG TCGGCTTCCG NCTGGAGGAT TCCTGAACCT      60
TCAAGCGCGG CCGATAACTG AGGTGCATCA TTAAGCGACT TTTCCAGAAC ATCCTGACGC      120
GCTCGAAACG CGGCACAGCC GACGGTGGCT CCGNCGAGGC GCTGNCTCCA AAATCCCTGA      180
GACAATTTCGN CGGGGGCGCC TACAAGGAAG TCGGTGCTGA ATTCGNCNG TATCTGGTCG      240
ACCTGTGTGG TCTGNAGCCG GACGAAGCGG TGCTCGACGT CG                        282

```

(2) INFORMATION FOR SEQ ID NO:106:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 3058 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

```

GATCGTACCC GTGCGAGTGC TCGGGCCGTT TGAGGATGGA GTGCACGTGT CTTTCGTGAT      60
GGCATACCCA GAGATGTTGG CGGCGGCGGC TGACACCCTG CAGAGCATCG GTGCTACCAC      120
TGTGGCTAGC AATGCCGCTG CGGCGGCCCC GACGACTGGG GTGGTGCCCC CCGCTGCCGA      180

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TGAGGTGTCTG	GCGCTGACTG	CGGCGCACTT	CGCCGCACAT	GCGGCGATGT	ATCAGTCCGT	240
GAGCGCTCGG	GCTGCTGCGA	TTCATGACCA	GTTCTGTGGC	ACCCTTGCCA	GCAGCGCCAG	300
CTCGTATGCG	GCCACTGAAG	TCGCCAATGC	GGCGGCGGCC	AGCTAAGCCA	GGAACAGTCG	360
GCACGAGAAA	CCACGAGAAA	TAGGGACACG	TAATGGTGGG	TTTCGGGGCG	TTACCACCGG	420
AGATCAACTC	CGCGAGGATG	TACGCCGGCC	CGGGTTCGGC	CTCGCTGGTG	GCCGCGGCTC	480
AGATGTGGGA	CAGCGTGGCG	AGTGACCTGT	TTTCGGCCGC	GTCGGCGTTT	CAGTCGGTGG	540
TCTGGGGTCT	GACGGTGGGG	TCGTGGATAG	GTTCTGTGGC	GGGTCTGATG	GTGGCGGCGG	600
CCTCGCCGTA	TGTGGCGTGG	ATGAGCGTCA	CCGCGGGGCA	GGCCGAGCTG	ACCGCCGCCC	660
AGGTCCGGGT	TGCTGCGGCG	GCCTACGAGA	CGGCGTATGG	GCTGACGGTG	CCCCCGCCGG	720
TGATCGCCGA	GAACCGTGCT	GAAGTATGA	TTCTGATAGC	GACCAACCTC	TTGGGGCAAA	780
ACACCCCGGC	GATCGCGGTC	AACGAGGCCG	AATACGGCGA	GATGTGGGCC	CAAGACGCCG	840
CCGCGATGTT	TGGCTACGCC	GCGGCGACGG	CGACGGCGAC	GGCGACGTTG	CTGCCGTTTCG	900
AGGAGGCGCC	GGAGATGACC	AGCGCGGGTG	GGCTCCTCGA	GCAGGCCGCC	GCGGTCGAGG	960
AGGCCTCCGA	CACCGCCGCG	GCGAACCAGT	TGATGAACAA	TGTGCCCCAG	GCGCTGCAAC	1020
AGCTGGCCCA	GCCCACGCAG	GGCACCACGC	CTTCTTCCAA	GCTGGGTGGC	CTGTGGAAGA	1080
CGGTCTCGCC	GCATCGGTCTG	CCGATCAGCA	ACATGGTGTC	GATGGCCAAC	AACCACATGT	1140
CGATGACCAA	CTCGGGTGTG	TCGATGACCA	ACACCTTGAG	CTCGATGTTG	AAGGGCTTTG	1200
CTCCGGCGGC	GGCCGCCCAG	GCCGTGCAAA	CCGCGGCGCA	AAACGGGGTC	CGGGCGATGA	1260
GCTCGCTGGG	CAGCTCGCTG	GGTTCTTCGG	GTCTGGGCGG	TGGGGTGGCC	GCCAACTTGG	1320
GTCGGGCGGC	CTCGGTTCGGT	TCGTTGTCTG	TGCCGCAGGC	CTGGGCGCGG	GCCAACCAGG	1380
CAGTCACCCC	GGCGGCGCGG	GCGCTGCCGC	TGACCAGCCT	GACCAGCGCC	GCGGAAAGAG	1440
GGCCCGGGCA	GATGCTGGGC	GGGCTGCCGG	TGGGGCAGAT	GGGCGCCAGG	GCCGGTGGTG	1500
GGCTCAGTGG	TGTGCTGCGT	GTTCCGCCGC	GACCCTATGT	GATGCCGCAT	TCTCCGGCGG	1560
CCGGCTAGGA	GAGGGGGCGC	AGACTGTCGT	TATTTGACCA	GTGATCGGCG	GTCTCGGTGT	1620
TTCCGCGGCC	GGCTATGACA	ACAGTCAATG	TGCATGACAA	GTTACAGGTA	TTAGGTCCAG	1680
GTTCAACAAG	GAGACAGGCA	ACATGGCCTC	ACGTTTTTATG	ACGGATCCGC	ACGCGATGCG	1740
GGACATGGCG	GGCCGTTTTG	AGGTGCACGC	CCAGACGGTG	GAGGACGAGG	CTCGCCGGAT	1800
GTGGGCGTCC	GCGCAAAACA	TTTCCGGTGC	GGGCTGGAGT	GGCATGGCCG	AGGCGACCTC	1860
GCTAGACACC	ATGGCCCAGA	TGAATCAGGC	GTTTCGCAAC	ATCGTGAACA	TGCTGCACGG	1920
GGTGCGTGAC	GGGCTGGTTC	GCGACGCCAA	CAACTACGAG	CAGCAAGAGC	AGGCCTCCCA	1980
GCAGATCCTC	AGCAGCTAAC	GTCAGCCGCT	GCAGCACAAT	ACTTTTACAA	GCGAAGGAGA	2040

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ACAGGTTCTGA TGACCATCAA CTATCAATTC GGGGATGTCG ACGCTCACGG CGCCATGATC 2100
CGCGCTCAGG CCGGGTTGCT GGAGGCCGAG CATCAGGCCA TCATTTCGTGA TGTGTTGACC 2160
GCGAGTGA CT TTTGGGGCGG CGCCGGTTCG GCGGCCTGCC AGGGGTTTCAT TACCCAGTTG 2220
GGCCGTA ACT TCCAGGTGAT CTACGAGCAG GCCAACGCCC ACGGGCAGAA GGTGCAGGCT 2280
GCCGGCAACA ACATGGCGCA AACCGACAGC GCCGTCGGCT CCAGCTGGGC CTGACACCAG 2340
GCCAAGGCCA GGGACGTGGT GTACGAGTGA AGTTCCTCGC GTGATCCTTC GGGTGGCAGT 2400
CTAAGTGGTC AGTGCTGGGG TGTGTTGGT TGTGCTGCTTG GCGGGTTCTT CGGTGCTGGT 2460
CAGTGCTGCT CGGGCTCGGG TGAGGACCTC GAGGCCCAGG TAGCGCCGTC CTTCGATCCA 2520
TTCGTCGTGT TGTTCGGCGA GGACGGCTCC GACGAGGCGG ATGATCGAGG CGCGGTCGGG 2580
GAAGATGCCC ACGACGTCGG TTCGGCGTCG TACCTCTCGG TTGAGGCGTT CCTGGGGGTT 2640
GTTGGACCAG ATTTGGCGCC AGATCTGCTT GGGGAAGGCG GTGAACGCCA GCAGGTCGGT 2700
GCGGGCGGTG TCGAGGTGCT CGGCCACCGC GGGGAGTTTG TCGGTCAGAG CGTCGAGTAC 2760
CCGATCATAT TGGGCAACAA CTGATTCGGC GTCGGGCTGG TCGTAGATGG AGTGCAGCAG 2820
GGTGCGCACC CACGGCCAGG AGGGCTTCGG GGTGGCTGCC ATCAGATTGG CTGCGTAGTG 2880
GGTTCTGCAG CGCTGCCAGG CCGCTGCGGG CAGGGTGGCG CCGATCGCGG CCACCAGGCC 2940
GGCGTGGGCG TCGCTGGTGA CCAGCGCGAC CCCGGACAGG CCGCGGGCGA CCAGGTCGCG 3000
GAAGAACGCC AGCCAGCCGG CCCCGTCCTC GGCGGAGGTG ACCTGGATGC CCAGGATC 3058

```

(2) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 391 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

```

Met Val Asp Phe Gly Ala Leu Pro Pro Glu Ile Asn Ser Ala Arg Met
1           5           10           15
Tyr Ala Gly Pro Gly Ser Ala Ser Leu Val Ala Ala Ala Gln Met Trp
          20           25           30
Asp Ser Val Ala Ser Asp Leu Phe Ser Ala Ala Ser Ala Phe Gln Ser
          35           40           45
Val Val Trp Gly Leu Thr Val Gly Ser Trp Ile Gly Ser Ser Ala Gly
          50           55           60
Leu Met Val Ala Ala Ala Ser Pro Tyr Val Ala Trp Met Ser Val Thr

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129

65		70		75		80
Ala Gly Gln Ala Glu Leu Thr Ala Ala Gln Val Arg Val Ala Ala Ala	85		90		95	
Ala Tyr Glu Thr Ala Tyr Gly Leu Thr Val Pro Pro Pro Val Ile Ala	100		105		110	
Glu Asn Arg Ala Glu Leu Met Ile Leu Ile Ala Thr Asn Leu Leu Gly	115		120		125	
Gln Asn Thr Pro Ala Ile Ala Val Asn Glu Ala Glu Tyr Gly Glu Met	130		135		140	
Trp Ala Gln Asp Ala Ala Ala Met Phe Gly Tyr Ala Ala Ala Thr Ala	145		150		155	160
Thr Ala Thr Ala Thr Leu Leu Pro Phe Glu Glu Ala Pro Glu Met Thr	165		170		175	
Ser Ala Gly Gly Leu Leu Glu Gln Ala Ala Ala Val Glu Glu Ala Ser	180		185		190	
Asp Thr Ala Ala Ala Asn Gln Leu Met Asn Asn Val Pro Gln Ala Leu	195		200		205	
Gln Gln Leu Ala Gln Pro Thr Gln Gly Thr Thr Pro Ser Ser Lys Leu	210		215		220	
Gly Gly Leu Trp Lys Thr Val Ser Pro His Arg Ser Pro Ile Ser Asn	225		230		235	240
Met Val Ser Met Ala Asn Asn His Met Ser Met Thr Asn Ser Gly Val	245		250		255	
Ser Met Thr Asn Thr Leu Ser Ser Met Leu Lys Gly Phe Ala Pro Ala	260		265		270	
Ala Ala Ala Gln Ala Val Gln Thr Ala Ala Gln Asn Gly Val Arg Ala	275		280		285	
Met Ser Ser Leu Gly Ser Ser Leu Gly Ser Ser Gly Leu Gly Gly Gly	290		295		300	
Val Ala Ala Asn Leu Gly Arg Ala Ala Ser Val Gly Ser Leu Ser Val	305		310		315	320
Pro Gln Ala Trp Ala Ala Ala Asn Gln Ala Val Thr Pro Ala Ala Arg	325		330		335	
Ala Leu Pro Leu Thr Ser Leu Thr Ser Ala Ala Glu Arg Gly Pro Gly	340		345		350	
Gln Met Leu Gly Gly Leu Pro Val Gly Gln Met Gly Ala Arg Ala Gly	355		360		365	
Gly Gly Leu Ser Gly Val Leu Arg Val Pro Pro Arg Pro Tyr Val Met	370		375		380	
Pro His Ser Pro Ala Ala Gly	385		390			

(2) INFORMATION FOR SEQ ID NO:108:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1725 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

GACGTCAGCA CCCGCCGTGC AGGGCTGGAG CGTGGTCGGT TTTGATCTGC GGTCAAGGTG	60
ACGTCCCTCG GCGTGTGCGC GGCGTGGATG CAGACTCGAT GCCGCTCTTT AGTGCAACTA	120
ATTTCTGTTGA AGTGCTGCG AGGTATAGGA CTTCACGATT GGTTAATGTA GCGTTCACCC	180
CGTGTTGGGG TCGATTTGGC CGGACCAGTC GTCACCAACG CTTGGCGTGC GCGCCAGGCG	240
GGCGATCAGA TCGCTTGACT ACCAATCAAT CTTGAGCTCC CGGGCCGATG CTCGGGCTAA	300
ATGAGGAGGA GCACGCGTGT CTTTCACTGC GCAACCGGAG ATGTTGGCGG CCGCGGCTGG	360
CGAACTTCGT TCCCTGGGGG CAACGCTGAA GGCTAGCAAT GCCGCCGAG CCGTGCCGAC	420
GACTGGGGTG GTGCCCCCGG CTGCCGACGA GGTGTCGCTG CTGCTTGCCA CACAATTCCG	480
TACGCATGCG GCGACGTATC AGACGGCCAG CGCCAAGGCC GCGGTGATCC ATGAGCAGTT	540
TGTGACCACG CTGGCCACCA GCGCTAGTTC ATATGCGGAC ACCGAGGCCG CCAACGCTGT	600
GGTCACCGGC TAGCTGACCT GACGGTATTC GAGCGGAAGG ATTATCGAAG TGGTGGATTT	660
CGGGGCGTTA CCACCGGAGA TCAACTCCGC GAGGATGTAC GCCGGCCCCG GTTCGGCCTC	720
GCTGGTGGCC GCCGCGAAGA TGTGGGACAG CGTGGCGAGT GACCTGTTTT CGGCCGCGTC	780
GGCGTTTCAG TCGGTGGTCT GGGGTCTGAC GGTGGGGTCG TGGATAGGTT CGTCGGCGGG	840
TCTGATGGCG GCGGCGGCCT CGCCGTATGT GGCGTGGATG AGCGTCACCG CGGGGCAGGC	900
CCAGCTGACC GCCGCCAGG TCCGGGTTGC TCGGCGGCC TACGAGACAG CGTATAGGCT	960
GACGGTGCCC CCGCCGGTGA TCGCCGAGAA CCGTACCGAA CTGATGACGC TGACCGCGAC	1020
CAACCTCTTG GGGCAAAACA CGCCGGCGAT CGAGGCCAAT CAGGCCGCAT ACAGCCAGAT	1080
GTGGGGCCAA GACGCGGAGG CGATGTATGG CTACGCCGCC ACGGCGGCGA CGGCGACCGA	1140
GGCGTTGCTG CCGTTCGAGG ACGCCCCACT GATACCAAC CCCGGCGGGC TCCTTGAGCA	1200
GGCCGTCGCG GTCGAGGAGG CCATCGACAC CGCCGCGGCG AACCAGTTGA TGAACAATGT	1260
GCCCCAAGCG CTGCAACAGC TGGCCCAGCC AGCGCAGGGC GTCGTACCTT CTTCCAAGCT	1320
GGGTGGGCTG TGGACGGCGG TCTCGCCGCA TCTGTGCGCG CTCAGCAACG TCAGTTTCAT	1380
AGCCAACAAC CACATGTCGA TGATGGGCAC GGGTGTGTGCG ATGACCAACA CCTTGCACTC	1440


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GATGTTGAAG GGCTTAGCTC CGGCGGCGGC TCAGGCCGTG GAAACCGCGG CGGAAAACGG      1500
GGTCTGGGCG ATGAGCTCGC TGGGCAGCCA GCTGGGTTCG TCGCTGGGTT CTTCGGGTCT      1560
GGGCGCTGGG GTGGCCGCCA ACTTGGGTCG GCGGCCTCG GTCGGTTCGT TGTCGGTGCC      1620
GCCAGCATGG GCCGCGGCCA ACCAGGCGGT CACCCCGGCG GCGCGGGCGC TGCCGCTGAC      1680
CAGCCTGACC AGCGCCGCCC AAACCGCCCC CGGACACATG CTGGG                        1725

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(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 359 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

```

Val Val Asp Phe Gly Ala Leu Pro Pro Glu Ile Asn Ser Ala Arg Met
1           5           10           15
Tyr Ala Gly Pro Gly Ser Ala Ser Leu Val Ala Ala Ala Lys Met Trp
20          25          30
Asp Ser Val Ala Ser Asp Leu Phe Ser Ala Ala Ser Ala Phe Gln Ser
35          40          45
Val Val Trp Gly Leu Thr Val Gly Ser Trp Ile Gly Ser Ser Ala Gly
50          55          60
Leu Met Ala Ala Ala Ala Ser Pro Tyr Val Ala Trp Met Ser Val Thr
65          70          75          80
Ala Gly Gln Ala Gln Leu Thr Ala Ala Gln Val Arg Val Ala Ala Ala
85          90          95
Ala Tyr Glu Thr Ala Tyr Arg Leu Thr Val Pro Pro Pro Val Ile Ala
100         105         110
Glu Asn Arg Thr Glu Leu Met Thr Leu Thr Ala Thr Asn Leu Leu Gly
115         120         125
Gln Asn Thr Pro Ala Ile Glu Ala Asn Gln Ala Ala Tyr Ser Gln Met
130         135         140
Trp Gly Gln Asp Ala Glu Ala Met Tyr Gly Tyr Ala Ala Thr Ala Ala
145         150         155         160
Thr Ala Thr Glu Ala Leu Leu Pro Phe Glu Asp Ala Pro Leu Ile Thr
165         170         175
Asn Pro Gly Gly Leu Leu Glu Gln Ala Val Ala Val Glu Glu Ala Ile
180         185         190
Asp Thr Ala Ala Ala Asn Gln Leu Met Asn Asn Val Pro Gln Ala Leu
195         200         205

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Gln Gln Leu Ala Gln Pro Ala Gln Gly Val Val Pro Ser Ser Lys Leu
 210 215 220
 Gly Gly Leu Trp Thr Ala Val Ser Pro His Leu Ser Pro Leu Ser Asn
 225 230 235 240
 Val Ser Ser Ile Ala Asn Asn His Met Ser Met Met Gly Thr Gly Val
 245 250 255
 Ser Met Thr Asn Thr Leu His Ser Met Leu Lys Gly Leu Ala Pro Ala
 260 265 270
 Ala Ala Gln Ala Val Glu Thr Ala Ala Glu Asn Gly Val Trp Ala Met
 275 280 285
 Ser Ser Leu Gly Ser Gln Leu Gly Ser Ser Leu Gly Ser Ser Gly Leu
 290 295 300
 Gly Ala Gly Val Ala Ala Asn Leu Gly Arg Ala Ala Ser Val Gly Ser
 305 310 315 320
 Leu Ser Val Pro Pro Ala Trp Ala Ala Ala Asn Gln Ala Val Thr Pro
 325 330 335
 Ala Ala Arg Ala Leu Pro Leu Thr Ser Leu Thr Ser Ala Ala Gln Thr
 340 345 350
 Ala Pro Gly His Met Leu Gly
 355

(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3027 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

AGTTCAGTCG AGAATGATAC TGACGGGCTG TATCCACGAT GGCTGAGACA ACCGAACCAC 60
 CGTCGGACGC GGGGACATCG CAAGCCGACG CGATGGCGTT GGCCGCCGAA GCCGAAGCCG 120
 CCGAAGCCGA AGCGCTGGCC GCCGCGGCGC GGGCCCGTGC CCGTGCCGCC CGGTTGAAGC 180
 GTGAGGCGCT GGCGATGGCC CCAGCCGAGG ACGAGAACGT CCCCAGGAT ATGCAGACTG 240
 GGAAGACGCC GAAGACTATG ACGACTATGA CGACTATGAG GCCGCAGACC AGGAGGCCGC 300
 ACGGTCGGCA TCCTGGCGAC GGCGGTTGCG GGTGCGGTTA CCAAGACTGT CCACGATTGC 360
 CATGGCGGCC GCAGTCGTCA TCATCTGCGG CTTACCGGG CTCAGCGGAT ACATTGTGTG 420
 GCAACACCAT GAGGCCACCG AACGCCAGCA GCGCGCCGCG GCGTTCGCCG CCGGAGCCAA 480
 GCAAGGTGTC ATCAACATGA CCTCGCTGGA CTTCAACAAG GCCAAAGAAG ACGTCGCGCG 540

TGTGATCGAC AGCTCCACCG GCGAATTCAG GGATGACTTC CAGCAGCGGG CAGCCGATTT	600
CACCAAGGTT GTCGAACAGT CCAAAGTGGT CACCGAAGGC ACGGTGAACG CGACAGCCGT	660
CGAATCCATG AACGAGCATT CCGCCGTGGT GCTCGTCGCG GCGACTTCAC GGGTCACCAA	720
TTCCGCTGGG GCGAAAGACG AACCACGTGC GTGGCGGCTC AAAGTGACCG TGACCGAAGA	780
GGGGGGACAG TACAAGATGT CGAAAGTTGA GTTCGTACCG TGACCGATGA CGTACGCGAC	840
GTCAACACCG AAACCACTGA CGCCACCGAA GTCGCTGAGA TCGACTCAGC CGCAGGCGAA	900
GCCGGTGATT CGGCGACCGA GGCATTTGAC ACCGACTCTG CAACGGAATC TACCGCGCAG	960
AAGGGTCAGC GGCACCGTGA CCTGTGGCGA ATGCAGGTTA CCTTGAAACC CGTTCCGGTG	1020
ATTCTCATCC TGCTCATGTT GATCTCTGGG GCGCGACGG GATGGCTATA CCTTGAGCAA	1080
TACGACCCGA TCAGCAGACG GACTCCGGCG CCGCCCGTGC TGCCGTCGCC GCGGCGTCTG	1140
ACGGGACAAT CGCGCTGTTG TGTATTCACC CGACACGTCG ACCAAGACTT CGCTACCGCC	1200
AGGTTCGACC TCGCCGGCGA TTTCTGTCC TATACGACCA GTTCACGCAG CAGATCGTGG	1260
CTCCGGCGGC CAAACAGAAG TCACTGAAAA CCACCGCCAA GGTGGTGCGC GCGGCCGTGT	1320
CGGAGCTACA TCCGGATTCG GCCGTGCTTC TGGTTTTTGT CGACCAGAGC ACTACCAGTA	1380
AGGACAGCCC CAATCCGTCG ATGGCGGCCA GCAGCGTGAT GGTGACCCTA GCCAAGGTCG	1440
ACGGCAATTG GCTGATCACC AAGTTCACCC CGGTTTAGGT TGCCGTAGGC GGTGCGCAAG	1500
TCTGACGGGG GCGCGGGTGG CTGCTCGTGC GAGATACCGG CCGTTCTCCG GACAATCACG	1560
GCCCGACCTC AAACAGATCT CGGCCGCTGT CTAATCGGCC GGGTTATTTA AGATTAGTTG	1620
CCACTGTATT TACCTGATGT TCAGATTGTT CAGCTGGATT TAGCTTCGCG GCAGGGCGGC	1680
TGGTGCACTT TGCATCTGGG GTTGTGACTA CTTGAGAGAA TTTGACCTGT TGCCGACGTT	1740
GTTTGCTGTC CATCATTGGT GCTAGTTATG GCCGAGCGGA AGGATTATCG AAGTGGTGGA	1800
CTTCGGGGCG TTACCACCGG AGATCAACTC CGCGAGGATG TACGCCGGCC CGGGTTCGGC	1860
CTCGCTGGTG GCCGCCGCGA AGATGTGGGA CAGCGTGGCG AGTGACCTGT TTTCCGCCGC	1920
GTCGGCGTTT CAGTCGGTGG TCTGGGGTCT GACGACGGGA TCGTGGATAG GTTCGTCGGC	1980
GGGTCTGATG GTGGCGGCGG CCTCGCCGTA TGTGGCGTGG ATGAGCGTCA CCGCGGGGCA	2040
GGCCGAGCTG ACCGCCGCC AGGTCCGGGT TGCTGCGGCG GCCTACGAGA CGGCGTATGG	2100
GCTGACGGTG CCCCCGCCG TGATCGCCGA GAACCGTGCT GAACTGATGA TTCTGATAGC	2160
GACCAACCTC TTGGGGCAAA ACACCCCGGC GATCGCGGTC AACGAGGCCG AATACGGGGA	2220
GATGTGGGCC CAAGACGCCG CCGCGATGTT TGGCTACGCC GCCACGGCGG CGACGGCGAC	2280
CGAGGCGTTG CTGCCGTTG AGGACGCCCC ACTGATCACC AACCCCGGCG GGCTCCTTGA	2340
GCAGGCCGTC GCGGTCGAGG AGGCCATCGA CACCGCCGCG GCGAACCAGT TGATGAACAA	2400

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TGTGCCCCAA GCGCTGCAAC AACTGGCCCA GCCCAGGAAA AGCATCTGGC CGTTCGACCA      2460
ACTGAGTGAA CTCTGGAAAG CCATCTCGCC GCATCTGTCTG CCGCTCAGCA ACATCGTGTCT      2520
GATGCTCAAC AACCACGTGT CGATGACCAA CTCGGGTGTG TCGATGGCCA GCACCTTGCA      2580
CTCAATGTTG AAGGGCTTTG CTCCGGCGGC GGCTCAGGCC GTGGAAACCG CGGCGCAAAA      2640
CGGGGTCCAG GCGATGAGCT CGCTGGGCAG CCAGCTGGGT TCGTCGCTGG GTTCTTCGGG      2700
TCTGGGCGCT GGGGTGGCCG CCAACTTGGG TCGGGCGGCC TCGGTCGGTT CGTTGTCTGGT      2760
GCCGCAGGCC TGGGCCGCGG CCAACCAGGC GGTCACCCCG GCGGCGCGGG CGCTGCCGCT      2820
GACCAGCCTG ACCAGCGCCG CCCAAACCGC CCCCAGACAC ATGCTGGGCG GGCTACCGCT      2880
GGGGCAACTG ACCAATAGCG GCGGCGGGTT CGGCGGGGTT AGCAATGCGT TGCGGATGCC      2940
GCCGCGGGCG TACGTAATGC CCCGTGTGCC CGCCGCCGGG TAACGCCGAT CCGCACGCAA      3000
TGCGGGCCCT CTATGCGGGC AGCGATC                                          3027

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(2) INFORMATION FOR SEQ ID NO:111:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 396 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

```

Val Val Asp Phe Gly Ala Leu Pro Pro Glu Ile Asn Ser Ala Arg Met
1           5           10           15
Tyr Ala Gly Pro Gly Ser Ala Ser Leu Val Ala Ala Ala Lys Met Trp
20        25        30
Asp Ser Val Ala Ser Asp Leu Phe Ser Ala Ala Ser Ala Phe Gln Ser
35        40        45
Val Val Trp Gly Leu Thr Thr Gly Ser Trp Ile Gly Ser Ser Ala Gly
50        55        60
Leu Met Val Ala Ala Ala Ser Pro Tyr Val Ala Trp Met Ser Val Thr
65        70        75        80
Ala Gly Gln Ala Glu Leu Thr Ala Ala Gln Val Arg Val Ala Ala Ala
85        90        95
Ala Tyr Glu Thr Ala Tyr Gly Leu Thr Val Pro Pro Pro Val Ile Ala
100       105       110
Glu Asn Arg Ala Glu Leu Met Ile Leu Ile Ala Thr Asn Leu Leu Gly
115      120      125
Gln Asn Thr Pro Ala Ile Ala Val Asn Glu Ala Glu Tyr Gly Glu Met

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135

130	135	140
Trp 145	Ala Gln Asp Ala Ala Ala Met Phe Gly Tyr 150	Ala Ala Thr Ala Ala 155 160
Thr 165	Ala Thr Glu Ala Leu Leu Pro Phe Glu Asp Ala Pro Leu Ile Thr 170 175	
Asn 180	Pro Gly Gly Leu Leu Glu Gln Ala Val Ala Val Glu Glu Ala Ile 185 190	
Asp 195	Thr Ala Ala Ala Asn Gln Leu Met Asn Asn Val Pro Gln Ala Leu 200 205	
Gln 210	Gln Leu Ala Gln Pro Thr Lys Ser Ile Trp Pro Phe Asp Gln Leu 215 220	
Ser 225	Glu Leu Trp Lys Ala Ile Ser Pro His Leu Ser Pro Leu Ser Asn 230 235 240	
Ile 245	Val Ser Met Leu Asn Asn His Val Ser Met Thr Asn Ser Gly Val 250 255	
Ser 260	Met Ala Ser Thr Leu His Ser Met Leu Lys Gly Phe Ala Pro Ala 265 270	
Ala 275	Ala Gln Ala Val Glu Thr Ala Ala Gln Asn Gly Val Gln Ala Met 280 285	
Ser 290	Ser Leu Gly Ser Gln Leu Gly Ser Ser Leu Gly Ser Ser Gly Leu 295 300	
Gly 305	Ala Gly Val Ala Ala Asn Leu Gly Arg Ala Ala Ser Val Gly Ser 310 315 320	
Leu 325	Ser Val Pro Gln Ala Trp Ala Ala Ala Asn Gln Ala Val Thr Pro 330 335	
Ala 340	Ala Arg Ala Leu Pro Leu Thr Ser Leu Thr Ser Ala Ala Gln Thr 345 350	
Ala 355	Pro Gly His Met Leu Gly Gly Leu Pro Leu Gly Gln Leu Thr Asn 360 365	
Ser 370	Gly Gly Gly Phe Gly Gly Val Ser Asn Ala Leu Arg Met Pro Pro 375 380	
Arg 385	Ala Tyr Val Met Pro Arg Val Pro Ala Ala Gly 390 395	

(2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1616 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

CATCGGAGGG AGTGATCACC ATGCTGTGGC ACGCAATGCC ACCGGAGTAA ATACCGCACG	60
GCTGATGGCC GGC GCGGGTC CGGCTCCAAT GCTTGCGGCG GCCGCGGGAT GGCAGACGCT	120
TTCGGCGGCT CTGGACGCTC AGGCCGTCGA GTTGACCGCG CGCCTGAACT CTCTGGGAGA	180
AGCCTGGACT GGAGGTGGCA GCGACAAGGC GCTTGCGGCT GCAACGCCGA TGGTGGTCTG	240
GCTACAAACC GCGTCAACAC AGGCCAAGAC CCGTGCGATG CAGGCGACGG CGCAAGCCGC	300
GGCATAACACC CAGGCCATGG CCACGACGCC GTCGCTGCCG GAGATCGCCG CCAACCACAT	360
CACCCAGGCC GTCCTTACGG CCACCAACTT CTTCGGTATC AACACGATCC CGATCGCGTT	420
GACCGAGATG GATTATTTCA TCCGTATGTG GAACCAGGCA GCCCTGGCAA TGGAGGTCTA	480
CCAGGCCGAG ACCGCGGTTA ACACGCTTTT CGAGAAGCTC GAGCCGATGG CGTCGATCCT	540
TGATCCCGGC GCGAGCCAGA GCACGACGAA CCCGATCTTC GGAATGCCCT CCCCTGGCAG	600
CTCAACACCG GTTGCCAGT TGCCGCCGGC GGCTACCCAG ACCCTCGGCC AACTGGGTGA	660
GATGAGCGGC CCGATGCAGC AGCTGACCCA GCCGCTGCAG CAGGTGACGT CGTTGTTCAG	720
CCAGGTGGGC GGCACCGGCG GCGGCAACCC AGCCGACGAG GAAGCCGCGC AGATGGGCCT	780
GCTCGGCACC AGTCCGCTGT CGAACCATCC GCTGGCTGGT GGATCAGGCC CCAGCGCGGG	840
CGCGGGCCTG CTGCGCGCGG AGTCGCTACC TGGCGCAGGT GGGTCGTTGA CCCGCACGCC	900
GCTGATGTCT CAGCTGATCG AAAAGCCGGT TGCCCCCTCG GTGATGCCGG CGGCTGCTGC	960
CGGATCGTCG GCGACGGGTG GCGCCGCTCC GGTGGGTGCG GGAGCGATGG GCCAGGGTGC	1020
GCAATCCGGC GGCTCCACCA GGCCGGGTCT GGTCGCGCCG GCACCGCTCG CGCAGGAGCG	1080
TGAAGAAGAC GACGAGGACG ACTGGGACGA AGAGGACGAC TGGTGAGCTC CCGTAATGAC	1140
AACAGACTTC CCGGCCACCC GGGCCGGAAG ACTTGCCAAC ATTTTGGCGA GGAAGGTAAA	1200
GAGAGAAAGT AGTCCAGCAT GGCAGAGATG AAGACCGATG CCGCTACCCT CGCGCAGGAG	1260
GCAGGTAATT TCGAGCGGAT CTCCGGCGAC CTGAAAACCC AGATCGACCA GGTGGAGTCG	1320
ACGGCAGGTT CGTTGCAGGG CCAGTGGCGC GGC GCGGCGG GGACGGCCGC CCAGGCCGCG	1380
GTGGTGCGCT TCCAAGAAGC AGCCAATAAG CAGAAGCAGG AACTCGACGA GATCTCGACG	1440
AATATTCGTC AGGCCGGCGT CCAATACTCG AGGGCCGACG AGGAGCAGCA GCAGGCGCTG	1500
TCCTCGCAA TGGGCTTCTG ACCCGCTAAT ACGAAAAGAA ACGGAGCAAA AACATGACAG	1560
AGCAGCAGTG GAATTCGCG GGTATCGAGG CCGCGGCAAG CGCAATCCAG GGAAAT	1616

(2) INFORMATION FOR SEQ ID NO:113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 432 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

CTAGTGGATG GGACCATGGC CATTTTCTGC AGTCTCACTG CCTTCTGTGT TGACATTTTG	60
GCACGCCGGC GGAAACGAAG CACTGGGGTC GAAGAACGGC TGCGCTGCCA TATCGTCCGG	120
AGCTTCCATA CCTTCGTGCG GCCGGAAGAG CTTGTCTGTAG TCGGCCGCCA TGACAACCTC	180
TCAGAGTGCG CTCAAACGTA TAAACACGAG AAAGGGCGAG ACCGACGGAA GGTCGAACTC	240
GCCCCATCCC GTGTTTCGCT ATTCTACGCG AACTCGGCGT TGCCCTATGC GAACATCCCA	300
GTGACGTTGC CTTGGGTCGA AGCCATTGCC TGACCGGCTT CGCTGATCGT CCGCGCCAGG	360
TTCTGCAGCG CGTTGTTTCTAG CTCGGTAGCC GTGGCGTCCC ATTTTGTCTG GACACCCTGG	420
TACGCCTCCG AA	432

(2) INFORMATION FOR SEQ ID NO:114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 368 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

Met Leu Trp His Ala Met Pro Pro Glu Xaa Asn Thr Ala Arg Leu Met	
1 5 10 15	
Ala Gly Ala Gly Pro Ala Pro Met Leu Ala Ala Ala Ala Gly Trp Gln	
20 25 30	
Thr Leu Ser Ala Ala Leu Asp Ala Gln Ala Val Glu Leu Thr Ala Arg	
35 40 45	
Leu Asn Ser Leu Gly Glu Ala Trp Thr Gly Gly Gly Ser Asp Lys Ala	
50 55 60	
Leu Ala Ala Ala Thr Pro Met Val Val Trp Leu Gln Thr Ala Ser Thr	
65 70 75 80	
Gln Ala Lys Thr Arg Ala Met Gln Ala Thr Ala Gln Ala Ala Ala Tyr	
85 90 95	
Thr Gln Ala Met Ala Thr Thr Pro Ser Leu Pro Glu Ile Ala Ala Asn	
100 105 110	
His Ile Thr Gln Ala Val Leu Thr Ala Thr Asn Phe Phe Gly Ile Asn	
115 120 125	

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Thr Ile Pro Ile Ala Leu Thr Glu Met Asp Tyr Phe Ile Arg Met Trp
130                      135                      140

Asn Gln Ala Ala Leu Ala Met Glu Val Tyr Gln Ala Glu Thr Ala Val
145                      150                      155                      160

Asn Thr Leu Phe Glu Lys Leu Glu Pro Met Ala Ser Ile Leu Asp Pro
165                      170                      175

Gly Ala Ser Gln Ser Thr Thr Asn Pro Ile Phe Gly Met Pro Ser Pro
180                      185                      190

Gly Ser Ser Thr Pro Val Gly Gln Leu Pro Pro Ala Ala Thr Gln Thr
195                      200                      205

Leu Gly Gln Leu Gly Glu Met Ser Gly Pro Met Gln Gln Leu Thr Gln
210                      215                      220

Pro Leu Gln Gln Val Thr Ser Leu Phe Ser Gln Val Gly Gly Thr Gly
225                      230                      235                      240

Gly Gly Asn Pro Ala Asp Glu Glu Ala Ala Gln Met Gly Leu Leu Gly
245                      250                      255

Thr Ser Pro Leu Ser Asn His Pro Leu Ala Gly Gly Ser Gly Pro Ser
260                      265                      270

Ala Gly Ala Gly Leu Leu Arg Ala Glu Ser Leu Pro Gly Ala Gly Gly
275                      280                      285

Ser Leu Thr Arg Thr Pro Leu Met Ser Gln Leu Ile Glu Lys Pro Val
290                      295                      300

Ala Pro Ser Val Met Pro Ala Ala Ala Ala Gly Ser Ser Ala Thr Gly
305                      310                      315                      320

Gly Ala Ala Pro Val Gly Ala Gly Ala Met Gly Gln Gly Ala Gln Ser
325                      330                      335

Gly Gly Ser Thr Arg Pro Gly Leu Val Ala Pro Ala Pro Leu Ala Gln
340                      345                      350

Glu Arg Glu Glu Asp Asp Glu Asp Asp Trp Asp Glu Glu Asp Asp Trp
355                      360                      365

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(2) INFORMATION FOR SEQ ID NO:115:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 100 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

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Met Ala Glu Met Lys Thr Asp Ala Ala Thr Leu Ala Gln Glu Ala Gly
1           5           10           15

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Asn Phe Glu Arg Ile Ser Gly Asp Leu Lys Thr Gln Ile Asp Gln Val
 20 25 30
 Glu Ser Thr Ala Gly Ser Leu Gln Gly Gln Trp Arg Gly Ala Ala Gly
 35 40 45
 Thr Ala Ala Gln Ala Ala Val Val Arg Phe Gln Glu Ala Ala Asn Lys
 50 55 60
 Gln Lys Gln Glu Leu Asp Glu Ile Ser Thr Asn Ile Arg Gln Ala Gly
 65 70 75 80
 Val Gln Tyr Ser Arg Ala Asp Glu Glu Gln Gln Gln Ala Leu Ser Ser
 85 90 95
 Gln Met Gly Phe
 100

(2) INFORMATION FOR SEQ ID NO:116:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 396 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

GATCTCCGGC GACCTGAAAA CCCAGATCGA CCAGGTGGAG TCGACGGCAG GTTCGTTGCA	60
GGGCCAGTGG CGCGGCGCGG CGGGGACGGC CGCCAGGCC GCGGTGGTGC GCTTCCAAGA	120
AGCAGCCAAT AAGCAGAAGC AGGAACTCGA CGAGATCTCG ACGAATATTC GTCAGGCCGG	180
CGTCCAATAC TCGAGGGCCG ACGAGGAGCA GCAGCAGGCG CTGTCCTCGC AAATGGGCTT	240
CTGACCCGCT AATACGAAAA GAAACGGAGC AAAAACATGA CAGAGCAGCA GTGGAATTTT	300
GCGGGTATCG AGGCCGCGGC AAGCGCAATC CAGGGAAATG TCACGTCCAT TCATTCCCTC	360
CTTGACGAGG GGAAGCAGTC CCTGACCAAG CTCGCA	396

(2) INFORMATION FOR SEQ ID NO:117:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 80 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

Ile Ser Gly Asp Leu Lys Thr Gln Ile Asp Gln Val Glu Ser Thr Ala

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1	5	10	15
Gly Ser Leu Gln Gly Gln Trp Arg Gly Ala Ala Gly Thr Ala Ala Gln	20	25	30
Ala Ala Val Val Arg Phe Gln Glu Ala Ala Asn Lys Gln Lys Gln Glu	35	40	45
Leu Asp Glu Ile Ser Thr Asn Ile Arg Gln Ala Gly Val Gln Tyr Ser	50	55	60
Arg Ala Asp Glu Glu Gln Gln Gln Ala Leu Ser Ser Gln Met Gly Phe	65	70	75
			80

(2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 387 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

GTGGATCCCG ATCCCGTGTT TCGCTATTCT ACGCGAACTC GGC GTTGCCC TATGCGAACA	60
TCCCAGTGAC GTTGCCCTTCG GTCGAAGCCA TTGCCTGACC GGCTTCGCTG ATCGTCCGCG	120
CCAGGTTCTG CAGCGCGTTG TTCAGCTCGG TAGCCGTGGC GTCCCATTTT TGCTGGACAC	180
CCTGGTACGC CTCCGAACCG CTACCGCCCC AGGCCGCTGC GAGCTTGGTC AGGGACTGCT	240
TCCCCTCGTC AAGGAGGGAA TGAATGGACG TGACATTTCC CTGGATTGCG CTTGCCGCGG	300
CCTCGATACC CGCGAAATTC CACTGCTGCT CTGTCATGTT TTTGCTCCGT TTCTTTTCGT	360
ATTAGCGGGT CAGAAGCCCA TTTGCGA	387

(2) INFORMATION FOR SEQ ID NO:119:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 272 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

CGGCACGAGG ATCTCGGTTG GCCCAACGGC GCTGGCGAGG GCTCCGTTCC GGGGGCGAGC	60
TGCGCGCCGG ATGCTTCCTC TGCCCGCAGC CGCGCCTGGA TGGATGGACC AGTTGCTACC	120
TTCCCGACGT TTCGTTCCGT GTCTGTGCGA TAGCGGTGAC CCCGGCGCGC ACGTCGGGAG	180

TGTTGGGGGG CAGGCCGGGT CGGTGGTTCG GCCGGGGACG CAGACGGTCT GGACGGAACG 240
GGCGGGGGGTT CGCCGATTGG CATCTTTGCC CA 272

(2) INFORMATION FOR SEQ ID NO:120:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

Asp Pro Val Asp Ala Val Ile Asn Thr Thr Cys Asn Tyr Gly Gln Val
1 5 10 15
Val Ala Ala Leu
20

(2) INFORMATION FOR SEQ ID NO:121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

Ala Val Glu Ser Gly Met Leu Ala Leu Gly Thr Pro Ala Pro Ser
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

Ala Ala Met Lys Pro Arg Thr Gly Asp Gly Pro Leu Glu Ala Ala Lys
1 5 10 15
Glu Gly Arg

(2) INFORMATION FOR SEQ ID NO:123:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 15 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

Tyr Tyr Trp Cys Pro Gly Gln Pro Phe Asp Pro Ala Trp Gly Pro
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:124:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 14 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

Asp Ile Gly Ser Glu Ser Thr Glu Asp Gln Gln Xaa Ala Val
1 5 10

(2) INFORMATION FOR SEQ ID NO:125:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 13 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

Ala Glu Glu Ser Ile Ser Thr Xaa Glu Xaa Ile Val Pro
1 5 10

(2) INFORMATION FOR SEQ ID NO:126:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

Asp Pro Glu Pro Ala Pro Pro Val Pro Thr Thr Ala Ala Ser Pro Pro
 1 5 10 15
 Ser

(2) INFORMATION FOR SEQ ID NO:127:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 15 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

Ala Pro Lys Thr Tyr Xaa Glu Glu Leu Lys Gly Thr Asp Thr Gly
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:128:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 30 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

Asp Pro Ala Ser Ala Pro Asp Val Pro Thr Ala Ala Gln Leu Thr Ser
 1 5 10 15
 Leu Leu Asn Ser Leu Ala Asp Pro Asn Val Ser Phe Ala Asn
 20 25 30

(2) INFORMATION FOR SEQ ID NO:129:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

Asp Pro Pro Asp Pro His Gln Xaa Asp Met Thr Lys Gly Tyr Tyr Pro
 1 5 10 15

Gly Gly Arg Arg Xaa Phe
20

(2) INFORMATION FOR SEQ ID NO:130:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

Asp Pro Gly Tyr Thr Pro Gly
1 5

(2) INFORMATION FOR SEQ ID NO:131:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ix) FEATURE:

(D) OTHER INFORMATION: /note= "The Second Residue Can Be Either a Pro or Thr"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

Xaa Xaa Gly Phe Thr Gly Pro Gln Phe Tyr
1 5 10

(2) INFORMATION FOR SEQ ID NO:132:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ix) FEATURE:

(D) OTHER INFORMATION: /note= "The Third Residue Can Be Either a Gln or Leu"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

Xaa Pro Xaa Val Thr Ala Tyr Ala Gly
1 5

(2) INFORMATION FOR SEQ ID NO:133:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 9 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

Xaa Xaa Xaa Glu Lys Pro Phe Leu Arg
1 5

(2) INFORMATION FOR SEQ ID NO:134:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

Xaa Asp Ser Glu Lys Ser Ala Thr Ile Lys Val Thr Asp Ala Ser
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:135:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 15 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

Ala Gly Asp Thr Xaa Ile Tyr Ile Val Gly Asn Leu Thr Ala Asp
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:136:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

Ala Pro Glu Ser Gly Ala Gly Leu Gly Gly Thr Val Gln Ala Gly
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:137:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

Xaa Tyr Ile Ala Tyr Xaa Thr Thr Ala Gly Ile Val Pro Gly Lys Ile
1 5 10 15

Asn Val His Leu Val
20

(2) INFORMATION FOR SEQ ID NO:138:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 882 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

GCAACGCTGT CGTGGCCTTT GCGGTGATCG GTTTCGCCTC GCTGGCGGTG GCGGTGGCGG	60
TCACCATCCG ACCGACCGCG GCCTCAAAAC CGGTAGAGGG ACACCAAAAC GCCCAGCCAG	120
GGAAGTTCAT GCCGTTGTTG CCGACGCAAC AGCAGGCGCC GGTCCCGCCG CCTCCGCCCCG	180
ATGATCCCAC CGCTGGATTC CAGGGCGGCA CCATTCCGGC TGTACAGAAC GTGGTGCCGC	240
GGCCGGGTAC CTCACCCGGG GTGGGTGGGA CGCCGGCTTC GCCTGCGCCG GAAGCGCCGG	300
CCGTGCCCCG TGTTGTGCCT GCCCCGGTGC CAATCCCGGT CCCGATCATC ATTCCCCCGT	360
TCCCGGGTTG GCAGCCTGGA ATGCCGACCA TCCCCACCGC ACGCCGACG ACGCCGGTGA	420
CCACGTCGGC GACGACGCCG CCGACCACGC CGCCGACCAC GCCGGTGACC ACGCCGCCAA	480
CGACGCCGCC GACCACGCCG GTGACCACGC CGCCAACGAC GCCGCCGACC ACGCCGGTGA	540
CCACGCCACC AACGACCGTC GCCCCGACGA CCGTCGCCCC GACGACGGTC GCTCCGACCA	600
CCGTCGCCCC GACCACGGTC GCTCCAGCCA CCGCCACGCC GACGACCGTC GCTCCGCAGC	660

CGACGCAGCA GCCCAGCAA CAACCAACCC AACAGATGCC AACCCAGCAG CAGACCGTGG	720
CCCCGCAGAC GGTGGCGCCG GCTCCGCAGC CGCCGTCCGG TGGCCGCAAC GGCAGCGGCG	780
GGGGCGACTT ATTCGGCGGG TTCTGATCAC GGTCGCGGCT TCACTACGGT CGGAGGACAT	840
GGCCGGTGAT GCGGTGACGG TGGTGCTGCC CTGTCTCAAC GA	882

(2) INFORMATION FOR SEQ ID NO:139:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 815 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

CCATCAACCA ACCGCTCGCG CCGCCGCGC CGCCGGATCC GCCGTCGCCG CCACGCCCGC	60
CGGTGCCTCC GGTGCCCCCG TTGCCGCCGT CGCCGCCGTC GCCGCCGACC GGCTGGGTGC	120
CTAGGGCGCT GTTACCGCCC TGGTTGGCGG GGACGCCGCC GGCACCACCG GTACCGCCGA	180
TGGCGCCGTT GCCGCCGCG GCACCGTTGC CACCGTTGCC ACCGTTGCCA CCGTTGCCGA	240
CCAGCCACCC GCCGCGACCA CCGGCACCGC CGGCGCCGCC CGCACCGCCG GCGTGCCCGT	300
TCGTGCCCCGT ACCGCCGGCA CCGCCGTTGC CGCCGTCACC GCCGACGGAA CTACCGGCGG	360
ACGCGGCCTG CCCGCCGCG CCGCCCGCAC CGCCATTGGC ACCGCCGTCA CCGCCGGCTG	420
GGAGTGCCGC GATTAGGGCA CTGACCGGCG CAACCAGCGC AAGTACTCTC GGTCACCGAG	480
CACTTCCAGA CGACACCACA GCACGGGGTT GTCGGCGGAC TGGGTGAAAT GGCAGCCGAT	540
AGCGGCTAGC TGTCGGCTGC GGTCAACCTC GATCATGATG TCGAGGTGAC CGTGACCGCG	600
CCCCCGAAG GAGGCGCTGA ACTCGGCGTT GAGCCGATCG GCGATCGGTT GGGGCAGTGC	660
CCAGGCCAAT ACGGGGATAC CGGGTGTGNA AGCCGCCGCG AGCGCAGCTT CGGTTGCGCG	720
ACNGTGGTCG GGGTGGCCTG TTACGCCGTT GTCNTCGAAC ACGAGTAGCA GGTCTGCTCC	780
GGCGAGGGCA TCCACCACGC GTTGCGTCAG CTCGT	815

(2) INFORMATION FOR SEQ ID NO:140:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1152 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

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ACCAGCCGCC GGCTGAGGTC TCAGATCAGA GAGTCTCCGG ACTCACC GGG GCGGTTTCAGC      60
CTTCTCCAG AACAACTGCT GAAGATCCTC GCGCGCGAAA CAGGCGCTGA TTTGACGCTC      120
TATGACCGGT TGAACGACGA GATCATCCGG CAGATTGATA TGGCACC GCT GGGCTAACAG      180
GTGCGCAAGA TGGTGCAGCT GTATGTCTCG GACTCCGTGT CGCGGATCAG CTTTGCCGAC      240
GGCCGGGTGA TCGTGTGGAG CGAGGAGCTC GCGGAGAGCC AGTATCCGAT CGAGACGCTG      300
GACGGCATCA CGCTGTTTGG GCGGCCGACG ATGACAACGC CCTTCATCGT TGAGATGCTC      360
AAGCGTGAGC GCGACATCCA GCTCTTCACG ACCGACGGCC ACTACCAGGG CCGGATCTCA      420
ACACCCGACG TGTCATACGC GCCGCGGCTC CGTCAGCAAG TTCACCGCAC CGACGATCCT      480
GCGTTCTGCC TGTCGTTAAG CAAGCGGATC GTGTCGAGGA AGATCCTGAA TCAGCAGGCC      540
TTGATTCGGG CACACACGTC GGGGCAAGAC GTTGCTGAGA GCATCCGCAC GATGAAGCAC      600
TCGCTGGCCT GGGTCGATCG ATCGGGCTCC CTGGCGGAGT TGAACGGGTT CGAGGGAAAT      660
GCCGCAAAGG CATACTTCAC CGCGCTGGGG CATCTCGTCC CGCAGGAGTT CGCATTCAG      720
GGCCGCTCGA CTCGGCCGCC GTTGGACGCC TTCAACTCGA TGGTCAGCCT CGGCTATTCTG      780
CTGCTGTACA AGAACATCAT AGGGGCGATC GAGCGTCACA GCCTGAACGC GTATATCGGT      840
TTCCTACACC AGGATTCACG AGGGCACGCA ACGTCTCGTG CCGAATTCGG CACGAGCTCC      900
GCTGAAACCG CTGGCCGGCT GCTCAGTGCC CGTACGTAAT CCGCTGCGCC CAGGCCGGCC      960
CGCCGGCCGA ATACCAGCAG ATCGGACAGC GAATTGCCGC CCAGCCGGTT GGAGCCGTGC      1020
ATACCGCCGG CACACTCACC GGCAGCGAAC AGGCCTGGCA CCGTGGCGGC GCCGGTGTCC      1080
GCGTCTACTT CGACACCGCC CATCACGTAG TGACACGTG GCGCGACTTC CATTGCCTGC      1140
GTTTCGGCACG AG                                                    1152

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(2) INFORMATION FOR SEQ ID NO:141:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 655 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

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CTCGTGCCGA TTCGGCAGGG TGTACTTGCC GGTGGTGTAN GCCGCATGAG TGCCGACGAC      60
CAGCAATGCG GCAACAGCAC GGATCCCGGT CAACGACGCC ACCCGGTCCA CGTGGGCGAT      120

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CCGCTCGAGT CCGCCCTGGG CGGCTCTTTC CTTGGGCAGG GTCATCCGAC GTGTTTCCGC      180
CGTGGTTTGC CGCCATTATG CCGGCGCGCC GCGTCGGGCG GCCGGTATGG CCGAANGTCG      240
ATCAGCACAC CCGAGATACG GGTCTGTGCA AGCTTTTTGA GCGTCGCGCG GGGCAGCTTC      300
GCCGGCAATT CTACTAGCGA GAAGTCTGGC CCGATACGGA TCTGACCGAA GTCGCTGCGG      360
TGCAGCCCAC CCTCATTGGC GATGGCGCCG ACGATGGCGC CTGGACCGAT CTTGTGCCGC      420
TTGCCGACGG CGACGCGGTA GGTGGTCAAG TCCGGTCTAC GCTTGGGCCT TTGCGGACGG      480
TCCCCGACGCT GGTGCGGGTT GCGCCGCGAA AGCGGCGGGT CGGGTGCCAT CAGGAATGCC      540
TCACCGCCGC GGCCTGCAC GGCCAGTGCC GCGGCGATGT CAGCCATCGG GACATCATGC      600
TCGCGTTCAT ACTCCTCGAC CAGTCGGCGG AACAGCTCGA TTCCCGGACC GCCCA          655

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(2) INFORMATION FOR SEQ ID NO:142:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 267 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

```

Asn Ala Val Val Ala Phe Ala Val Ile Gly Phe Ala Ser Leu Ala Val
1           5           10           15
Ala Val Ala Val Thr Ile Arg Pro Thr Ala Ala Ser Lys Pro Val Glu
20          25          30
Gly His Gln Asn Ala Gln Pro Gly Lys Phe Met Pro Leu Leu Pro Thr
35          40          45
Gln Gln Gln Ala Pro Val Pro Pro Pro Pro Asp Asp Pro Thr Ala
50          55          60
Gly Phe Gln Gly Gly Thr Ile Pro Ala Val Gln Asn Val Val Pro Arg
65          70          75          80
Pro Gly Thr Ser Pro Gly Val Gly Gly Thr Pro Ala Ser Pro Ala Pro
85          90          95
Glu Ala Pro Ala Val Pro Gly Val Val Pro Ala Pro Val Pro Ile Pro
100         105         110
Val Pro Ile Ile Ile Pro Pro Phe Pro Gly Trp Gln Pro Gly Met Pro
115         120         125
Thr Ile Pro Thr Ala Pro Pro Thr Thr Pro Val Thr Thr Ser Ala Thr
130         135         140
Thr Pro Pro Thr Thr Pro Pro Thr Thr Pro Val Thr Thr Pro Pro Thr

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150

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145              150              155              160
Thr Pro Pro Thr Thr Pro Val Thr Thr Pro Pro Thr Thr Pro Pro Thr
              165              170              175
Thr Pro Val Thr Thr Pro Pro Thr Thr Val Ala Pro Thr Thr Val Ala
              180              185              190
Pro Thr Thr Val Ala Pro Thr Thr Val Ala Pro Thr Thr Val Ala Pro
              195              200              205
Ala Thr Ala Thr Pro Thr Thr Val Ala Pro Gln Pro Thr Gln Gln Pro
              210              215              220
Thr Gln Gln Pro Thr Gln Gln Met Pro Thr Gln Gln Gln Thr Val Ala
225              230              235              240
Pro Gln Thr Val Ala Pro Ala Pro Gln Pro Pro Ser Gly Gly Arg Asn
              245              250              255
Gly Ser Gly Gly Gly Asp Leu Phe Gly Gly Phe
              260              265

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(2) INFORMATION FOR SEQ ID NO:143:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

```

Ile Asn Gln Pro Leu Ala Pro Pro Ala Pro Pro Asp Pro Pro Ser Pro
1      5      10      15
Pro Arg Pro Pro Val Pro Pro Val Pro Pro Leu Pro Pro Ser Pro Pro
20     25     30
Ser Pro Pro Thr Gly Trp Val Pro Arg Ala Leu Leu Pro Pro Trp Leu
35     40     45
Ala Gly Thr Pro Pro Ala Pro Pro Val Pro Pro Met Ala Pro Leu Pro
50     55     60
Pro Ala Ala Pro Leu Pro Pro Leu Pro Pro Leu Pro Pro Leu Pro Thr
65     70     75     80
Ser His Pro Pro Arg Pro Pro Ala Pro Pro Ala Pro Pro Ala Pro Pro
85     90     95
Ala Cys Pro Phe Val Pro Val Pro Pro Ala Pro Pro Leu Pro Pro Ser
100    105    110
Pro Pro Thr Glu Leu Pro Ala Asp Ala Ala Cys Pro Pro Ala Pro Pro
115    120    125

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151

Ala Pro Pro Leu Ala Pro Pro Ser Pro Pro Ala Gly Ser Ala Ala Ile
 130 135 140

Arg Ala Leu Thr Gly Ala Thr Ser Ala Ser Thr Leu Gly His Arg Ala
 145 150 155 160

Leu Pro Asp Asp Thr Thr Ala Arg Gly Cys Arg Arg Thr Gly
 165 170

(2) INFORMATION FOR SEQ ID NO:144:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 35 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

Gln Pro Pro Ala Glu Val Ser Asp Gln Arg Val Ser Gly Leu Thr Gly
 1 5 10 15

Ala Val Gln Pro Ser Pro Arg Thr Thr Ala Glu Asp Pro Arg Pro Arg
 20 25 30

Asn Arg Arg
 35

(2) INFORMATION FOR SEQ ID NO:145:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 104 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

Arg Ala Asp Ser Ala Gly Cys Thr Cys Arg Trp Cys Xaa Pro His Glu
 1 5 10 15

Cys Arg Arg Pro Ala Met Arg Gln Gln His Gly Ser Arg Ser Thr Thr
 20 25 30

Pro Pro Gly Pro Arg Gly Arg Ser Ala Arg Val Arg Pro Gly Arg Leu
 35 40 45

Phe Pro Trp Ala Gly Ser Ser Asp Val Phe Pro Pro Trp Phe Ala Ala
 50 55 60

Ile Met Pro Ala Arg Arg Val Gly Arg Pro Val Trp Pro Xaa Val Asp
 65 70 75 80

Gln His Thr Arg Asp Thr Gly Leu Cys Lys Leu Phe Glu Arg Arg Ala
85 90 95

Gly Gln Leu Arg Arg Gln Phe Tyr
100

(2) INFORMATION FOR SEQ ID NO:146:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 53 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "PCR primer"
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

GGATCCATAT GGGCCATCAT CATCATCATC ACGTGATCGA CATCATCGGG ACC

53

(2) INFORMATION FOR SEQ ID NO:147:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 42 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "PCR Primer"
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

CCTGAATTCA GGCCTCGGTT GCGCCGGCCT CATCTTGAAC GA

42

(2) INFORMATION FOR SEQ ID NO:148:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "PCR Primer"
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

GGATCCTGCA GGCTCGAAAC CACCGAGCGG T

31

(2) INFORMATION FOR SEQ ID NO:149:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "PCR primer"

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

CTCTGAATTC AGCGCTGGAA ATCGTCGCGA T

31

(2) INFORMATION FOR SEQ ID NO:150:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "PCR primer"

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

GGATCCAGCG CTGAGATGAA GACCGATGCC GCT

33

(2) INFORMATION FOR SEQ ID NO:151:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "PCR primer"

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

GAGAGAATTC TCAGAAGCCC ATTTGCGAGG ACA

33

(2) INFORMATION FOR SEQ ID NO:152:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1993 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Mycobacterium tuberculosis

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 152..1273

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

TGTTCTTCGA CGGCAGGCTG GTGGAGGAAG GGCCACCGA ACAGCTGTTT TCCTCGCCGA	60
AGCATGCGGA AACCGCCCGA TACGTCGCCG GACTGTCGGG GGACGTCAAG GACGCCAAGC	120
GCGGAAATTG AAGAGCACAG AAAGGTATGG C GTG AAA ATT CGT TTG CAT ACG	172
Val Lys Ile Arg Leu His Thr	
1 5	
CTG TTG GCC GTG TTG ACC GCT GCG CCG CTG CTG CTA GCA GCG GCG GGC	220
Leu Leu Ala Val Leu Thr Ala Ala Pro Leu Leu Leu Ala Ala Ala Gly	
10 15 20	
TGT GGC TCG AAA CCA CCG AGC GGT TCG CCT GAA ACG GGC GCC GGC GCC	268
Cys Gly Ser Lys Pro Pro Ser Gly Ser Pro Glu Thr Gly Ala Gly Ala	
25 30 35	
GGT ACT GTC GCG ACT ACC CCC GCG TCG TCG CCG GTG ACG TTG GCG GAG	316
Gly Thr Val Ala Thr Thr Pro Ala Ser Ser Pro Val Thr Leu Ala Glu	
40 45 50 55	
ACC GGT AGC ACG CTG CTC TAC CCG CTG TTC AAC CTG TGG GGT CCG GCC	364
Thr Gly Ser Thr Leu Leu Tyr Pro Leu Phe Asn Leu Trp Gly Pro Ala	
60 65 70	
TTT CAC GAG AGG TAT CCG AAC GTC ACG ATC ACC GCT CAG GGC ACC GGT	412
Phe His Glu Arg Tyr Pro Asn Val Thr Ile Thr Ala Gln Gly Thr Gly	
75 80 85	
TCT GGT GCC GGG ATC GCG CAG GCC GCC GCC GGG ACG GTC AAC ATT GGG	460
Ser Gly Ala Gly Ile Ala Gln Ala Ala Ala Gly Thr Val Asn Ile Gly	
90 95 100	
GCC TCC GAC GCC TAT CTG TCG GAA GGT GAT ATG GCC GCG CAC AAG GGG	508
Ala Ser Asp Ala Tyr Leu Ser Glu Gly Asp Met Ala Ala His Lys Gly	
105 110 115	
CTG ATG AAC ATC GCG CTA GCC ATC TCC GCT CAG CAG GTC AAC TAC AAC	556
Leu Met Asn Ile Ala Leu Ala Ile Ser Ala Gln Gln Val Asn Tyr Asn	
120 125 130 135	

CTG CCC GGA GTG AGC GAG CAC CTC AAG CTG AAC GGA AAA GTC CTG GCG Leu Pro Gly Val Ser Glu His Leu Lys Leu Asn Gly Lys Val Leu Ala 140 145 150	604
GCC ATG TAC CAG GGC ACC ATC AAA ACC TGG GAC GAC CCG CAG ATC GCT Ala Met Tyr Gln Gly Thr Ile Lys Thr Trp Asp Asp Pro Gln Ile Ala 155 160 165	652
GCG CTC AAC CCC GGC GTG AAC CTG CCC GGC ACC GCG GTA GTT CCG CTG Ala Leu Asn Pro Gly Val Asn Leu Pro Gly Thr Ala Val Val Pro Leu 170 175 180	700
CAC CGC TCC GAC GGG TCC GGT GAC ACC TTC TTG TTC ACC CAG TAC CTG His Arg Ser Asp Gly Ser Gly Asp Thr Phe Leu Phe Thr Gln Tyr Leu 185 190 195	748
TCC AAG CAA GAT CCC GAG GGC TGG GGC AAG TCG CCC GGC TTC GGC ACC Ser Lys Gln Asp Pro Glu Gly Trp Gly Lys Ser Pro Gly Phe Gly Thr 200 205 210 215	796
ACC GTC GAC TTC CCG GCG GTG CCG GGT GCG CTG GGT GAG AAC GGC AAC Thr Val Asp Phe Pro Ala Val Pro Gly Ala Leu Gly Glu Asn Gly Asn 220 225 230	844
GGC GGC ATG GTG ACC GGT TGC GCC GAG ACA CCG GGC TGC GTG GCC TAT Gly Gly Met Val Thr Gly Cys Ala Glu Thr Pro Gly Cys Val Ala Tyr 235 240 245	892
ATC GGC ATC AGC TTC CTC GAC CAG GCC AGT CAA CGG GGA CTC GGC GAG Ile Gly Ile Ser Phe Leu Asp Gln Ala Ser Gln Arg Gly Leu Gly Glu 250 255 260	940
GCC CAA CTA GGC AAT AGC TCT GGC AAT TTC TTG TTG CCC GAC GCG CAA Ala Gln Leu Gly Asn Ser Ser Gly Asn Phe Leu Leu Pro Asp Ala Gln 265 270 275	988
AGC ATT CAG GCC GCG GCG GCT GGC TTC GCA TCG AAA ACC CCG GCG AAC Ser Ile Gln Ala Ala Ala Gly Phe Ala Ser Lys Thr Pro Ala Asn 280 285 290 295	1036
CAG GCG ATT TCG ATG ATC GAC GGG CCC GCC CCG GAC GGC TAC CCG ATC Gln Ala Ile Ser Met Ile Asp Gly Pro Ala Pro Asp Gly Tyr Pro Ile 300 305 310	1084
ATC AAC TAC GAG TAC GCC ATC GTC AAC AAC CGG CAA AAG GAC GCC GCC Ile Asn Tyr Glu Tyr Ala Ile Val Asn Asn Arg Gln Lys Asp Ala Ala 315 320 325	1132
ACC GCG CAG ACC TTG CAG GCA TTT CTG CAC TGG GCG ATC ACC GAC GGC Thr Ala Gln Thr Leu Gln Ala Phe Leu His Trp Ala Ile Thr Asp Gly 330 335 340	1180
AAC AAG GCC TCG TTC CTC GAC CAG GTT CAT TTC CAG CCG CTG CCG CCC Asn Lys Ala Ser Phe Leu Asp Gln Val His Phe Gln Pro Leu Pro Pro 345 350 355	1228
GCG GTG GTG AAG TTG TCT GAC GCG TTG ATC GCG ACG ATT TCC AGC Ala Val Val Lys Leu Ser Asp Ala Leu Ile Ala Thr Ile Ser Ser 360 365 370	1273
TAGCCTCGTT GACCACCACG CGACAGCAAC CTCCGTCGGG CCATCGGGCT GCTTTGCGGA	1333

GCATGCTGGC CCGTGCCGGT GAAGTCGGCC GCGCTGGCCC GGCCATCCGG TGGTTGGGTG 1393
 GGATAGGTGC GGTGATCCCG CTGCTTGCGC TGGTCTTGGT GCTGGTGGTG CTGGTCATCG 1453
 AGGCGATGGG TGCATCAGG CTCAACGGGT TGCATTTCTT CACCGCCACC GAATGGAATC 1513
 CAGGCAACAC CTACGGCGAA ACCGTTGTCA CCGACGCGTC GCCCATCCGG TCGGCGCCTA 1573
 CTACGGGGCG TTGCCGCTGA TCGTCGGGAC GCTGGCGACC TCGGCAATCG CCCTGATCAT 1633
 CGCGGTGCCG GTCTCTGTAG GAGCGGCGCT GGTGATCGTG GAACGGCTGC CGAAACGGTT 1693
 GGCCGAGGCT GTGGGAATAG TCCTGGAATT GCTCGCCGGA ATCCCCAGCG TGGTCGTCGG 1753
 TTTGTGGGGG GCAATGACGT TCGGGCCGTT CATCGCTCAT CACATCGCTC CGGTGATCGC 1813
 TCACAACGCT CCCGATGTGC CGGTGCTGAA CTACTTGCGC GGCGACCCGG GCAACGGGGA 1873
 GGGCATGTTG GTGTCCGGTC TGGTGTTGGC GGTGATGGTC GTTCCCATTA TCGCCACCAC 1933
 CACTCATGAC CTGTTCCGGC AGGTGCCGGT GTTGCCCCGG GAGGGCGCGA TCGGGAATTC 1993

(2) INFORMATION FOR SEQ ID NO:153:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 374 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

Val Lys Ile Arg Leu His Thr Leu Leu Ala Val Leu Thr Ala Ala Pro
 1 5 10 15
 Leu Leu Leu Ala Ala Ala Gly Cys Gly Ser Lys Pro Pro Ser Gly Ser
 20 25 30
 Pro Glu Thr Gly Ala Gly Ala Gly Thr Val Ala Thr Thr Pro Ala Ser
 35 40 45
 Ser Pro Val Thr Leu Ala Glu Thr Gly Ser Thr Leu Leu Tyr Pro Leu
 50 55 60
 Phe Asn Leu Trp Gly Pro Ala Phe His Glu Arg Tyr Pro Asn Val Thr
 65 70 75 80
 Ile Thr Ala Gln Gly Thr Gly Ser Gly Ala Gly Ile Ala Gln Ala Ala
 85 90 95
 Ala Gly Thr Val Asn Ile Gly Ala Ser Asp Ala Tyr Leu Ser Glu Gly
 100 105 110
 Asp Met Ala Ala His Lys Gly Leu Met Asn Ile Ala Leu Ala Ile Ser
 115 120 125
 Ala Gln Gln Val Asn Tyr Asn Leu Pro Gly Val Ser Glu His Leu Lys
 130 135 140

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Leu Asn Gly Lys Val Leu Ala Ala Met Tyr Gln Gly Thr Ile Lys Thr
 145 150 155 160
 Trp Asp Asp Pro Gln Ile Ala Ala Leu Asn Pro Gly Val Asn Leu Pro
 165 170 175
 Gly Thr Ala Val Val Pro Leu His Arg Ser Asp Gly Ser Gly Asp Thr
 180 185 190
 Phe Leu Phe Thr Gln Tyr Leu Ser Lys Gln Asp Pro Glu Gly Trp Gly
 195 200 205
 Lys Ser Pro Gly Phe Gly Thr Thr Val Asp Phe Pro Ala Val Pro Gly
 210 215 220
 Ala Leu Gly Glu Asn Gly Asn Gly Gly Met Val Thr Gly Cys Ala Glu
 225 230 235 240
 Thr Pro Gly Cys Val Ala Tyr Ile Gly Ile Ser Phe Leu Asp Gln Ala
 245 250 255
 Ser Gln Arg Gly Leu Gly Glu Ala Gln Leu Gly Asn Ser Ser Gly Asn
 260 265 270
 Phe Leu Leu Pro Asp Ala Gln Ser Ile Gln Ala Ala Ala Gly Phe
 275 280 285
 Ala Ser Lys Thr Pro Ala Asn Gln Ala Ile Ser Met Ile Asp Gly Pro
 290 295 300
 Ala Pro Asp Gly Tyr Pro Ile Ile Asn Tyr Glu Tyr Ala Ile Val Asn
 305 310 315 320
 Asn Arg Gln Lys Asp Ala Ala Thr Ala Gln Thr Leu Gln Ala Phe Leu
 325 330 335
 His Trp Ala Ile Thr Asp Gly Asn Lys Ala Ser Phe Leu Asp Gln Val
 340 345 350
 His Phe Gln Pro Leu Pro Pro Ala Val Val Lys Leu Ser Asp Ala Leu
 355 360 365
 Ile Ala Thr Ile Ser Ser
 370

(2) INFORMATION FOR SEQ ID NO:154:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1993 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

TGTTCTTCGA CGGCAGGCTG GTGGAGGAAG GGCCACCGA ACAGCTGTTC TCCTCGCCGA

AGCATGCGGA	AACCGCCCGA	TACGTCGCCG	GACTGTCGGG	GGACGTCAAG	GACGCCAAGC	120
GCGGAAATTG	AAGAGCACAG	AAAGGTATGG	CGTGAAAATT	CGTTTGCATA	CGCTGTTGGC	180
CGTGTTGACC	GCTGCGCCGC	TGCTGCTAGC	AGCGGCGGGC	TGTGGCTCGA	AACCACCGAG	240
CGGTTCGCCT	GAAACGGGCG	CCGGCGCCGG	TACTGTCGCG	ACTACCCCCG	CGTCGTCGCC	300
GGTGACGTTG	GCGGAGACCG	GTAGCACGCT	GCTCTACCCG	CTGTTCAACC	TGTGGGGTCC	360
GGCCTTTCAC	GAGAGGTATC	CGAACGTCAC	GATCACCGCT	CAGGGCACCG	GTTCTGGTGC	420
CGGGATCGCG	CAGGCCGCCG	CCGGGACGGT	CAACATTGGG	GCCTCCGACG	CCTATCTGTC	480
GGAAGGTGAT	ATGGCCGCGC	ACAAGGGGCT	GATGAACATC	GCGCTAGCCA	TCTCCGCTCA	540
GCAGGTCAAC	TACAACCTGC	CCGGAGTGAG	CGAGCACCTC	AAGCTGAACG	GAAAAGTCCT	600
GGCGGCCATG	TACCAGGGCA	CCATCAAAAC	CTGGGACGAC	CCGCAGATCG	CTGCGCTCAA	660
CCCCGGCGTG	AACCTGCCCG	GCACCGCGGT	AGTTCCGCTG	CACCGCTCCG	ACGGGTCCGG	720
TGACACCTTC	TTGTTACCCC	AGTACCTGTC	CAAGCAAGAT	CCCGAGGGCT	GGGGCAAGTC	780
GCCCCGGCTTC	GGCACCACCG	TCGACTTCCC	GGCGGTGCCG	GGTGCGCTGG	GTGAGAACGG	840
CAACGGCGGC	ATGGTGACCG	GTTGCGCCGA	GACACCGGGC	TGCGTGGCCT	ATATCGGCAT	900
CAGCTTCCTC	GACCAGGCCA	GTCAACGGGG	ACTCGGCGAG	GCCCAACTAG	GCAATAGCTC	960
TGGCAATTTT	TTGTTGCCCG	ACGCGCAAAG	CATTTCAGGCC	GCGGCGGCTG	GCTTCGCATC	1020
GAAAACCCCG	GCGAACCAGG	CGATTTCGAT	GATCGACGGG	CCCGCCCCGG	ACGGCTACCC	1080
GATCATCAAC	TACGAGTACG	CCATCGTCAA	CAACCGGCAA	AAGGACGCCG	CCACCGCGCA	1140
GACCTTGACG	GCATTTCTGC	ACTGGGCGAT	CACCGACGGC	AACAAGGCCT	CGTTCTCTCGA	1200
CCAGGTTTCAT	TTCCAGCCGC	TGCCGCCCCG	GGTGGTGAAG	TTGTCTGACG	CGTTGATCGC	1260
GACGATTTCC	AGCTAGCCTC	GTTGACCACC	ACGCGACAGC	AACCTCCGTC	GGGCCATCGG	1320
GCTGCTTTGC	GGAGCATGCT	GGCCCGTGCC	GGTGAAGTCG	GCCGCGCTGG	CCCGGCCATC	1380
CGGTGGTTGG	GTGGGATAGG	TGCGGTGATC	CCGCTGCTTG	CGCTGGTCTT	GGTGCTGGTG	1440
GTGCTGGTCA	TCGAGGCGAT	GGGTGCGATC	AGGCTCAACG	GGTTGCATTT	CTTCACCGCC	1500
ACCGAATGGA	ATCCAGGCAA	CACCTACGGC	GAAACCGTTG	TCACCGACGC	GTCGCCCATC	1560
CGGTCGGCGC	CTACTACGGG	GCGTTGCCGC	TGATCGTCGG	GACGCTGGCG	ACCTCGGCAA	1620
TCGCCCTGAT	CATCGCGGTG	CCGGTCTCTG	TAGGAGCGGC	GCTGGTGATC	GTGGAACGGC	1680
TGCCGAAACG	GTTGGCCGAG	GCTGTGGGAA	TAGTCCTGGA	ATTGCTCGCC	GGAATCCCCA	1740
GCGTGGTCGT	CGGTTTGTGG	GGGGCAATGA	CGTTCGGGCC	GTTTCATCGCT	CATCACATCG	1800
CTCCGGTGAT	CGCTCACAAAC	GCTCCCGATG	TGCCGGTGCT	GAACACTTTG	CGCGGCGACC	1860
CGGGCAACGG	GGAGGGCATG	TTGGTGTCCG	GTCTGGTGTT	GGCGGTGATG	GTCGTTCCCA	1920

TTATCGCCAC CACCACTCAT GACCTGTTCC GGCAGGTGCC GGTGTTGCCC CGGGAGGGCG 1980
 CGATCGGGAA TTC 1993

(2) INFORMATION FOR SEQ ID NO:155:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 374 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

Met Lys Ile Arg Leu His Thr Leu Leu Ala Val Leu Thr Ala Ala Pro
 1 5 10 15
 Leu Leu Leu Ala Ala Ala Gly Cys Gly Ser Lys Pro Pro Ser Gly Ser
 20 25 30
 Pro Glu Thr Gly Ala Gly Ala Gly Thr Val Ala Thr Thr Pro Ala Ser
 35 40 45
 Ser Pro Val Thr Leu Ala Glu Thr Gly Ser Thr Leu Leu Tyr Pro Leu
 50 55 60
 Phe Asn Leu Trp Gly Pro Ala Phe His Glu Arg Tyr Pro Asn Val Thr
 65 70 75 80
 Ile Thr Ala Gln Gly Thr Gly Ser Gly Ala Gly Ile Ala Gln Ala Ala
 85 90 95
 Ala Gly Thr Val Asn Ile Gly Ala Ser Asp Ala Tyr Leu Ser Glu Gly
 100 105 110
 Asp Met Ala Ala His Lys Gly Leu Met Asn Ile Ala Leu Ala Ile Ser
 115 120 125
 Ala Gln Gln Val Asn Tyr Asn Leu Pro Gly Val Ser Glu His Leu Lys
 130 135 140
 Leu Asn Gly Lys Val Leu Ala Ala Met Tyr Gln Gly Thr Ile Lys Thr
 145 150 155 160
 Trp Asp Asp Pro Gln Ile Ala Ala Leu Asn Pro Gly Val Asn Leu Pro
 165 170 175
 Gly Thr Ala Val Val Pro Leu His Arg Ser Asp Gly Ser Gly Asp Thr
 180 185 190
 Phe Leu Phe Thr Gln Tyr Leu Ser Lys Gln Asp Pro Glu Gly Trp Gly
 195 200 205
 Lys Ser Pro Gly Phe Gly Thr Thr Val Asp Phe Pro Ala Val Pro Gly
 210 215 220
 Ala Leu Gly Glu Asn Gly Asn Gly Gly Met Val Thr Gly Cys Ala Glu
 225 230 235 240

160

Thr Pro Gly Cys Val Ala Tyr Ile Gly Ile Ser Phe Leu Asp Gln Ala
 245 250 255
 Ser Gln Arg Gly Leu Gly Glu Ala Gln Leu Gly Asn Ser Ser Gly Asn
 260 265 270
 Phe Leu Leu Pro Asp Ala Gln Ser Ile Gln Ala Ala Ala Gly Phe
 275 280 285
 Ala Ser Lys Thr Pro Ala Asn Gln Ala Ile Ser Met Ile Asp Gly Pro
 290 295 300
 Ala Pro Asp Gly Tyr Pro Ile Ile Asn Tyr Glu Tyr Ala Ile Val Asn
 305 310 315 320
 Asn Arg Gln Lys Asp Ala Ala Thr Ala Gln Thr Leu Gln Ala Phe Leu
 325 330 335
 His Trp Ala Ile Thr Asp Gly Asn Lys Ala Ser Phe Leu Asp Gln Val
 340 345 350
 His Phe Gln Pro Leu Pro Pro Ala Val Val Lys Leu Ser Asp Ala Leu
 355 360 365
 Ile Ala Thr Ile Ser Ser
 370

(2) INFORMATION FOR SEQ ID NO:156:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1777 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

GGTCTTGACC ACCACCTGGG TGTCGAAGTC GGTGCCCGGA TTGAAGTCCA GGTACTCGTG	60
GGTGGGGCGG GCGAAACAAT AGCGACAAGC ATGCGAGCAG CCGCGGTAGC CGTTGACGGT	120
GTAGCGAAAC GGCAACGCGG CCGCGTTGGG CACCTTGTTT AGCGCTGATT TGCACAACAC	180
CTCGTGGAAG GTGATGCCGT CGAATTGTGG CGCGCGAACG CTGCGGACCA GGCCGATCCG	240
CTGCAACCCG GCAGCGCCCG TCGTCAACGG GCATCCCGTT CACCGCGACG GCTTGCCGGG	300
CCCAACGCAT ACCATTATTC GAACAACCGT TCTATACTTT GTCAACGCTG GCCGCTACCG	360
AGCGCCGCAC AGGATGTGAT ATGCCATCTC TGCCCGCACA GACAGGAGCC AGGCCTTATG	420
ACAGCATTCG GCGTCGAGCC CTACGGGCAG CCGAAGTACC TAGAAATCGC CGGGAAGCGC	480
ATGGCGTATA TCGACGAAGG CAAGGGTGAC GCCATCGTCT TTCAGCACGG CAACCCACG	540
TCGTCTTACT TGTGGCGCAA CATCATGCCG CACTTGGAAG GGCTGGGCCG GCTGGTGGCC	600

TGCGATCTGA TCGGGATGGG CGCGTCGGAC AAGCTCAGCC CATCGGGACC CGACCGCTAT	660
AGCTATGGCG AGCAACGAGA CTTTTTGTTC GCGCTCTGGG ATGCGCTCGA CCTCGGCGAC	720
CACGTGGTAC TGGTGCTGCA CGACTGGGGC TCGGCGCTCG GCTTCGACTG GGCTAACCAG	780
CATCGCGACC GAGTGCAGGG GATCGCGTTC ATGGAAGCGA TCGTCACCCC GATGACGTGG	840
GCGGACTGGC CGCCGGCCGT GCGGGGTGTG TTCCAGGGTT TCCGATCGCC TCAAGGCGAG	900
CCAATGGCGT TGGAGCACAA CATCTTTGTC GAACGGGTGC TGCCCGGGGC GATCCTGCGA	960
CAGCTCAGCG ACGAGGAAAT GAACCACTAT CGGCGGCCAT TCGTGAACGG CGGCGAGGAC	1020
CGTCGCCCCA CGTTGTCTGT GCCACGAAAC CTTCCAATCG ACGGTGAGCC CGCCGAGGTC	1080
GTCGCGTTGG TCAACGAGTA CCGGAGCTGG CTCGAGGAAA CCGACATGCC GAAACTGTTC	1140
ATCAACGCCG AGCCCGGCGC GATCATCACC GGCCGCATCC GTGACTATGT CAGGAGCTGG	1200
CCCAACCAGA CCGAAATCAC AGTGCCCGGC GTGCATTTTCG TTCAGGAGGA CAGCGATGGC	1260
GTCGTATCGT GGGCGGGCGC TCGGCAGCAT CGGCGACCTG GGAGCGCTCT CATTTACGA	1320
GACCAAGAAT GTGATTTCCG GCGAAGGCGG CGCCCTGCTT GTCAACTCAT AAGACTTCCT	1380
GCTCCGGGCA GAGATTCTCA GGGAAAAGGG CACCAATCGC AGCCGCTTCC TTCGCAACGA	1440
GGTCGACAAA TATACGTGGC AGGACAAAGG TCTTCCTATT TGCCCAGCGA ATTAGTCGCT	1500
GCCTTTCTAT GGGCTCAGTT CGAGGAAGCC GAGCGGATCA CGCGTATCCG ATTGGACCTA	1560
TGGAACCGGT ATCATGAAAG CTTCGAATCA TTGGAACAGC GGGGGCTCCT GCGCCGTCGG	1620
ATCATCCAC AGGGCTGCTC TCACAACGCC CACATGTACT ACGTGTTACT AGCGCCAGC	1680
GCCGATCGGG AGGAGGTGCT GCGCGTCTG ACGAGCGAAG GTATAGGCGC GGTCTTTCAT	1740
TACGTGCCGC TTCACGATTC GCCGGCCGGG CGTCGCT	1777

(2) INFORMATION FOR SEQ ID NO:157:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 324 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:

GAGATTGAAT CGTACCGGTC TCCTTAGCGG CTCCGTCCCG TGAATGCCCA TATCACGCAC	60
GGCCATGTTC TGGCTGTCGA CCTTCGCCCC ATGCCCGGAC GTTGGTAAAC CCAGGGTTTG	120
ATCAGTAATT CCGGGGGACG GTTGCGGGAA GGCGGCCAGG ATGTGCGTGA GCCGCGGCGC	180
CGCCGTCGCC CAGGCGACCG CTGGATGCTC AGCCCCGGTG CGGCGACGTA GCCAGCGTTT	240

GGCGCGTGTC GTCCACAGTG GTACTCCGGT GACGACGCGG CGCGGTGCCT GGGTGAAGAC	300
CGTGACCGAC GCCGCCGATT CAGA	324

(2) INFORMATION FOR SEQ ID NO:158:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1338 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

CGCGTACCGC CGCGTTGCGC TGGCACGGGA CCTGTACGAC CTGAACCACT TCGCCTCGCG	60
AACGATTGAC GAACCGCTCG TCGGCGGGCT GTGGGTGCTC AAGGTGTGGG GTGATGTCGT	120
CGATGACCGG CGCGGCACCC GGCCACTACG CGTCGAAGAC GTCCTCGCCG CCCGCAGCGA	180
GCACGACTTC CAGCCCGACT CGATCGGCGT GCTGACCCGT CCTGTGCTA TGGCTGCCTG	240
GGAAGCTCGC GTTCGGAAGC GATTTGCGTT CCTCACTGAC CTCGACGCCG ACGAGCAGCG	300
GTGGGCCGCC TCGACGAAC GGCACCGCCG CGAAGTGGAG AACGCGCTGG CGGTGCTGCG	360
GTCCTGATCA ACCTGCCGGC GATCGTGCCG TTCCGCTGGC ACGGTTGCGG CTGGACGCGG	420
CTGAATCGAC TAGATGAGAG CAGTTGGGCA CGAATCCGGC TGTGGTGGTG AGCAAGACAC	480
GAGTACTGTC ATCACTATTG GATGCACTGG ATGACCGGCC TGATTCAGCA GGACCAATGG	540
AACTGCCCCG GGCAAAACGT CTCGGAGATG ATCGGCGTCC CCTCGGAACC CTGCGGTGCT	600
GGCGTCATTC GGACATCGGT CCGGCTCGCG GGATCGTGGT GACGCCAGCG CTGAAGGAGT	660
GGAGCGCGGC GGTGCACGCG CTGCTGGACG GCCGGCAGAC GGTGCTGCTG CGTAAGGGCG	720
GGATCGGCGA GAAGCGCTTC GAGGTGGCGG CCCACGAGTT CTTGTTGTTC CCGACGGTCG	780
CGCACAGCCA CGCCGAGCGG GTTCGCCCCG AGCACC GCGA CCTGCTGGGC CCGGCGGCCG	840
CCGACAGCAC CGACGAGTGT GTGCTACTGC GGGCCG CAGC GAAAGTTGTT GCCGCACTGC	900
CGGTTAACCG GCCAGAGGGT CTGGACGCCA TCGAGGATCT GCACATCTGG ACCGCCGAGT	960
CGGTGCGCGC CGACCGGCTC GACTTTCGGC CCAAGCACAA ACTGGCCGTC TTGGTGGTCT	1020
CGGCGATCCC GCTGGCCGAG CCGGTCCGGC TGGCGCGTAG GCCCGAGTAC GGCGGTTGCA	1080
CCAGCTGGGT GCAGCTGCCG GTGACGCCGA CGTTGGCGGC GCCGGTGCAC GACGAGGCCG	1140
CGCTGGCCGA GGTGCGCGCC CGGGTCCGCG AGGCCGTGGG TTGACTGGGC GGCATCGCTT	1200
GGGTCTGAGC TGTACGCCCA GTCGGCGCTG CGAGTGATCT GCTGTCGGTT CCGTCCCTGC	1260
TGGCGTCAAT TGACGGCGCG GGCAACAGCA GCATTGGCGG CGCCATCCTC CGCGCGGCCG	1320

GCGCCCACCG CTACAACC

1338

(2) INFORMATION FOR SEQ ID NO:159:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 321 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

CCGGCGGCAC CGGCGGCACC GCGGGTACCG GCGGCAACGG CGCTGACGCC GCTGCTGTGG	60
TGGGCTTCGG CGCGAACGGC GACCCTGGCT TCGCTGGCGG CAAAGGCGGT AACGGCGGAA	120
TAGGTGGGGC CGCGGTGACA GCGGGGGTCG CCGGCGACGG CGGCACCGGC GGCAAAGGTG	180
GCACCGGCGG TGCCGGCGGC GCCGGCAACG ACGCCGGCAG CACCGGCAAT CCCGGCGGTA	240
AGGGCGGCGA CGGCGGGATC GCGGGTGCCG GCGGGGCCGG CGGCGCGGCC GGCACCGGCA	300
ACGGCGGCCA TGCCGGCAAC C	321

(2) INFORMATION FOR SEQ ID NO:160:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 492 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

GAAGACCCGG CCCCGCCATA TCGATCGGCT CGCCGACTAC TTTCGCCGAA CGTGACGCG	60
GCGGCGTCGG GCTGATCATC ACCGGTGGCT ACGCGCCCAA CCGCACCGGA TGGCTGCTGC	120
CGTTCGCCTC CGAACTCGTC ACTTCGGCGC AAGCCCCGACG GCACCGCCGA ATCACCAGGG	180
CGGTCCACGA TTCGGGTGCA AAGATCCTGC TGCAAATCCT GCACGCCGGA CGCTACGCCT	240
ACCACCCACT TGCGGTCAGC GCCTCGCCGA TCAAGGCGCC GATCACCCCG TTTCGTCCGC	300
GAGCACTATC GGCTCGCGGG GTCGAAGCGA CCATCGCGGA TTTCGCCCCG TGCGCGCAGT	360
TGGCCCGCGA TGCCGGCTAC GACGGCGTCG AAATCATGGG CAGCGAAGGG TATCTGCTCA	420
ATCAGTTCCT GGCGCCGCGC ACCAACAAGC GCACCGACTC GTGGGGCGGC ACACCGGCCA	480
ACCGTCGCCG GT	492

(2) INFORMATION FOR SEQ ID NO:161:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 536 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:

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Phe Ala Gln His Leu Val Glu Gly Asp Ala Val Glu Leu Trp Arg Ala
1           5           10           15
Asn Ala Ala Asp Gln Ala Asp Pro Leu Gln Pro Gly Ser Ala Arg Arg
20           25           30
Gln Arg Ala Ser Arg Ser Pro Arg Arg Leu Ala Gly Pro Asn Ala Tyr
35           40           45
His Tyr Ser Asn Asn Arg Ser Ile Leu Cys Gln Arg Trp Pro Leu Pro
50           55           60
Ser Ala Ala Gln Asp Val Ile Cys His Leu Cys Pro His Arg Gln Glu
65           70           75           80
Pro Gly Leu Met Thr Ala Phe Gly Val Glu Pro Tyr Gly Gln Pro Lys
85           90           95
Tyr Leu Glu Ile Ala Gly Lys Arg Met Ala Tyr Ile Asp Glu Gly Lys
100          105          110
Gly Asp Ala Ile Val Phe Gln His Gly Asn Pro Thr Ser Ser Tyr Leu
115          120          125
Trp Arg Asn Ile Met Pro His Leu Glu Gly Leu Gly Arg Leu Val Ala
130          135          140
Cys Asp Leu Ile Gly Met Gly Ala Ser Asp Lys Leu Ser Pro Ser Gly
145          150          155          160
Pro Asp Arg Tyr Ser Tyr Gly Glu Gln Arg Asp Phe Leu Phe Ala Leu
165          170          175
Trp Asp Ala Leu Asp Leu Gly Asp His Val Val Leu Val Leu His Asp
180          185          190
Trp Gly Ser Ala Leu Gly Phe Asp Trp Ala Asn Gln His Arg Asp Arg
195          200          205
Val Gln Gly Ile Ala Phe Met Glu Ala Ile Val Thr Pro Met Thr Trp
210          215          220
Ala Asp Trp Pro Pro Ala Val Arg Gly Val Phe Gln Gly Phe Arg Ser
225          230          235          240
Pro Gln Gly Glu Pro Met Ala Leu Glu His Asn Ile Phe Val Glu Arg
245          250          255
Val Leu Pro Gly Ala Ile Leu Arg Gln Leu Ser Asp Glu Glu Met Asn
260          265          270

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His Tyr Arg Arg Pro Phe Val Asn Gly Gly Glu Asp Arg Arg Pro Thr
 275 280 285
 Leu Ser Trp Pro Arg Asn Leu Pro Ile Asp Gly Glu Pro Ala Glu Val
 290 295 300
 Val Ala Leu Val Asn Glu Tyr Arg Ser Trp Leu Glu Glu Thr Asp Met
 305 310 315 320
 Pro Lys Leu Phe Ile Asn Ala Glu Pro Gly Ala Ile Ile Thr Gly Arg
 325 330 335
 Ile Arg Asp Tyr Val Arg Ser Trp Pro Asn Gln Thr Glu Ile Thr Val
 340 345 350
 Pro Gly Val His Phe Val Gln Glu Asp Ser Asp Gly Val Val Ser Trp
 355 360 365
 Ala Gly Ala Arg Gln His Arg Arg Pro Gly Ser Ala Leu Ile Ser Arg
 370 375 380
 Asp Gln Glu Cys Asp Phe Arg Arg Arg Arg Arg Pro Ala Cys Gln Leu
 385 390 395 400
 Ile Arg Leu Pro Ala Pro Gly Arg Asp Ser Gln Gly Lys Gly His Gln
 405 410 415
 Ser Gln Pro Leu Pro Ser Gln Arg Gly Arg Gln Ile Tyr Val Ala Gly
 420 425 430
 Gln Arg Ser Ser Tyr Leu Pro Ser Glu Leu Val Ala Ala Phe Leu Trp
 435 440 445
 Ala Gln Phe Glu Glu Ala Glu Arg Ile Thr Arg Ile Arg Leu Asp Leu
 450 455 460
 Trp Asn Arg Tyr His Glu Ser Phe Glu Ser Leu Glu Gln Arg Gly Leu
 465 470 475 480
 Leu Arg Arg Pro Ile Ile Pro Gln Gly Cys Ser His Asn Ala His Met
 485 490 495
 Tyr Tyr Val Leu Leu Ala Pro Ser Ala Asp Arg Glu Glu Val Leu Ala
 500 505 510
 Arg Leu Thr Ser Glu Gly Ile Gly Ala Val Phe His Tyr Val Pro Leu
 515 520 525
 His Asp Ser Pro Ala Gly Arg Arg
 530 535

(2) INFORMATION FOR SEQ ID NO:162:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 284 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

Asn	Glu	Ser	Ala	Pro	Arg	Ser	Pro	Met	Leu	Pro	Ser	Ala	Arg	Pro	Arg	1	5	10	15
Tyr	Asp	Ala	Ile	Ala	Val	Leu	Leu	Asn	Glu	Met	His	Ala	Gly	His	Cys	20	25	30	
Asp	Phe	Gly	Leu	Val	Gly	Pro	Ala	Pro	Asp	Ile	Val	Thr	Asp	Ala	Ala	35	40	45	
Gly	Asp	Asp	Arg	Ala	Gly	Leu	Gly	Val	Asp	Glu	Gln	Phe	Arg	His	Val	50	55	60	
Gly	Phe	Leu	Glu	Pro	Ala	Pro	Val	Leu	Val	Asp	Gln	Arg	Asp	Asp	Leu	65	70	75	80
Gly	Gly	Leu	Thr	Val	Asp	Trp	Lys	Val	Ser	Trp	Pro	Arg	Gln	Arg	Gly	85	90	95	
Ala	Thr	Val	Leu	Ala	Ala	Val	His	Glu	Trp	Pro	Pro	Ile	Val	Val	His	100	105	110	
Phe	Leu	Val	Ala	Glu	Leu	Ser	Gln	Asp	Arg	Pro	Gly	Gln	His	Pro	Phe	115	120	125	
Asp	Lys	Asp	Val	Val	Leu	Gln	Arg	His	Trp	Leu	Ala	Leu	Arg	Arg	Ser	130	135	140	
Glu	Thr	Leu	Glu	His	Thr	Pro	His	Gly	Arg	Arg	Pro	Val	Arg	Pro	Arg	145	150	155	160
His	Arg	Gly	Asp	Asp	Arg	Phe	His	Glu	Arg	Asp	Pro	Leu	His	Ser	Val	165	170	175	
Ala	Met	Leu	Val	Ser	Pro	Val	Glu	Ala	Glu	Arg	Arg	Ala	Pro	Val	Val	180	185	190	
Gln	His	Gln	Tyr	His	Val	Val	Ala	Glu	Val	Glu	Arg	Ile	Pro	Glu	Arg	195	200	205	
Glu	Gln	Lys	Val	Ser	Leu	Leu	Ala	Ile	Ala	Ile	Ala	Val	Gly	Ser	Arg	210	215	220	
Trp	Ala	Glu	Leu	Val	Arg	Arg	Ala	His	Pro	Asp	Gln	Ile	Ala	Gly	His	225	230	235	240
Gln	Pro	Ala	Gln	Pro	Phe	Gln	Val	Arg	His	Asp	Val	Ala	Pro	Gln	Val	245	250	255	
Arg	Arg	Arg	Gly	Val	Ala	Val	Leu	Lys	Asp	Asp	Gly	Val	Thr	Leu	Ala	260	265	270	
Phe	Val	Asp	Ile	Arg	His	Ala	Leu	Pro	Gly	Asp	Phe	275	280						

(2) INFORMATION FOR SEQ ID NO:163:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 264 base pairs

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:

ATGAACATGT CGTCGGTGGT GGGTCGCAAG GCCTTTGCGC GATTCGCCGG CTACTCCTCC	60
GCCATGCACG CGATCGCCGG TTTCTCCGAT GCGTTGCGCC AAGAGCTGCG GGGTAGCGGA	120
ATCGCCGTCT CGGTGATCCA CCCGGCGCTG ACCCAGACAC CGCTGTTGGC CAACGTCGAC	180
CCCGCCGACA TGCCGCCGCC GTTTCGCAGC CTCACGCCCA TTCCCGTTCA CTGGGTCGCG	240
GCAGCGGTGC TTGACGGTGT GGCG	264

(2) INFORMATION FOR SEQ ID NO:164:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1171 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

TAGTCGGCGA CGATGACGTC GCGGTCCAGG CCGACCGCTT CAAGCACCAG CGCGACCACG	60
AAGCCGGTGC GATCCTTACC CGCGAAGCAG TGGGTGAGCA CCGGGCGTCC GGCGGCAAGC	120
AGTGTGACGA CACGATGTAG CGCGCGCTGT GCTCCATTGC GCGTTGGGAA TTGGCGATAC	180
TCGTGCGTCA TGTAGCGGGT GGCCGCGTCA TTTATCGACT GGCTGGATTC GCCGGACTCG	240
CCGTTGGACC CGTCATTGGT TAGCAGCCTC TTGAATGCGG TTTCGTGCGG CGCTGAGTCG	300
TCGGCGTCAT CATCGGCGAG GTCGGGGAAC GGCAGCAGGT GGACGTCGAT GCCGTCCGGA	360
ACCCGTCCTG GACCGCGGCG GGCAACCTCC CGGGACGACC GCAGGTCGGC AACGTCGGTG	420
ATCCCCAGCC GGCGCAGCGT TGCCCCTCGT GCCGAATTCG GCACGAGGCT GGCGAGCCAC	480
CGGGCATCAC CAAGCAACGC TTGCCAGTA CGGATCGTCA CTTCCGCATC CGGCAGACCA	540
ATCTCCTCGC CGCCATCGT CAGATCCCGC TCGTGCGTTG ACAAGAACGG CCGCAGATGT	600
GCCAGCGGGT ATCGGAGATT GAACCGCGCA CGCAGTTCTT CAATCGCTGC GCGCTGCCGC	660
ACTATTGGCA CTTTCCGGCG GTCGCGGTAT TCAGCAAGCA TGCGAGTCTC GACGAACTCG	720
CCCCACGTAA CCCACGGCGT AGCTCCCGC GTGACGCGGA GGATCGGCGG GTGATCTTTG	780
CCGCCACGCT CGTAGCCGTT GATCCACCGC TTCGCGGTGC CGGCGGGGAG GCCGATCAGC	840

TTATCGACCT CGGCGTATGC CGACGGCAAG CTGGGCGCGT TCGTCGAGGT CAAGAACTCC	900
ACCATCGGCA CCGGCACCAA GGTGCCGCAC CTGACCTACG TCGGCGACGC CGACATCGGC	960
GAGTACAGCA ACATCGGCGC CTCCAGCGTG TTCGTCAACT ACGACGGTAC GTCCAAACGG	1020
CGCACCACCG TCGGTTTCGCA CGTACGGACC GGGTCCGACA CCATGTTCGT GGCCCCAGTA	1080
ACCATCGGCG ACGGCGCGTA TACCGGGGCC GGCACAGTGG TGCGGGAGGA TGTCCCGCCG	1140
GGGGCGCTGG CAGTGTCGGC GGGTCCGCAA C	1171

(2) INFORMATION FOR SEQ ID NO:165:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 227 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:

GCAAAGGCGG CACCGGCGGG GCCGGCATGA ACAGCCTCGA CCCGCTGCTA GCCGCCCAAG	60
ACGGCGGCCA AGGCGGCACC GGCGGCACCG GCGGCAACGC CGGCGCCGGC GGCACCAGCT	120
TCACCAAGG CGCCGACGGC AACGCCGGCA ACGGCGGTGA CGGCGGGGTC GGCGGCAACG	180
GCGGAAACGG CGGAAACGGC GCAGACAACA CCACCACCGC CGCCGCC	227

(2) INFORMATION FOR SEQ ID NO:166:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 304 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

CCTCGCCACC ATGGGCGGGC AGGGCGGTAG CGGTGGCGCC GGCTCTACCC CAGGCGCCAA	60
GGGCGCCAC GGCTTCACTC CAACCAGCGG CGGCGACGGC GGCACGGCG GCAACGGCGG	120
CAACTCCCAA GTGGTCGGCG GCAACGGCGG CGACGGCGGC AATGGCGGCA ACGGCGGCAG	180
CGCCGGCACG GCGGCAACG GCGGCCGCGG CGGCGACGGC GCGTTTGGTG GCATGAGTGC	240
CAACGCCACC AACCCTGGTG AAAACGGGCC AAACGGTAAC CCCGGCGGCA ACGGTGGCGC	300
CGGC	304

(2) INFORMATION FOR SEQ ID NO:167:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1439 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:167:

GTGGGACGCT GCCGAGGCTG TATAACAAGG ACAACATCGA CCAGCGCCGG CTCGGTGAGC	60
TGATCGACCT ATTTAACAGT GCGCGCTTCA GCCGGCAGGG CGAGCACCGC GCGGGGATC	120
TGATGGGTGA GGTCTACGAA TACTTCCTCG GCAATTTTCGC TCGCGCGGAA GGAAGCGGG	180
GTGGCGAGTT CTTTACCCCG CCCAGCGTGG TCAAGGTGAT CGTGGAGGTG CTGGAGCCGT	240
CGAGTGGGCG GGTGTATGAC CCGTGCTGCG GTTCCGGAGG CATGTTTGTG CAGACCGAGA	300
AGTTCATCTA CGAACACGAC GGCGATCCGA AGGATGTCTC GATCTATGGC CAGGAAAGCA	360
TTGAGGAGAC CTGGCGGATG GCGAAGATGA ACCTCGCCAT CCACGGCATC GACAACAAGG	420
GGCTCGGCGC CCGATGGAGT GATACCTTCG CCCGCGACCA GCACCCGGAC GTGCAGATGG	480
ACTACGTGAT GGCCAATCCG CCGTTCAACA TCAAAGACTG GGCCCGCAAC GAGGAAGACC	540
CACGCTGGCG CTTCGGTGTT CCGCCCGCCA ATAACGCCAA CTACGCATGG ATTCAGCACA	600
TCCTGTACAA CTTGGCGCCG GGAGGTCGGG CGGGCGTGGT GATGGCCAAC GGGTCGATGT	660
CGTCGAATC CAACGGCAAG GGGGATATTC GCGCGCAAAT CGTGGAGGCG GATTTGGTTT	720
CCTGCATGGT CGCGTTACCC ACCCAGCTGT TCCGCAGCAC CGGAATCCCG GTGTGCCTGT	780
GGTTTTTTCG CAAAAACAAG GCGGCAGGTA AGCAAGGGTC TATCAACCGG TGCGGGCAGG	840
TGCTGTTTCAT CGACGCTCGT GAACTGGGCG ACCTAGTGGA CCGGGCCGAG CGGGCGCTGA	900
CCAACGAGGA GATCGTCCGC ATCGGGGATA CCTTCCACGC GAGCACGACC ACCGGCAACG	960
CCGGCTCCGG TGGTGCCGGC GGTAATGGGG GCACTGGCCT CAACGGCGCG GGCGGTGCTG	1020
GCGGGGCCGG CGGCAACGCG GGTGTCGCCG GCGTGTCTTT CGGCAACGCT GTGGGCGGCG	1080
ACGGCGGCAA CGGCGGCAAC GGCGGCCACG GCGGCGACGG CACGACGGGC GGCGCCGGCG	1140
GCAAGGGCGG CAACGGCAGC AGCGGTGCCG CCAGCGGCTC AGGCGTCGTC AACGTCACCG	1200
CCGGCCACGG CGGCAACGGC GGCAATGGCG GCAACGGCGG CAACGGCTCC GCGGGCGCCG	1260
GCGGCCAGGG CGGTGCCGGC GGCAGCGCCG GCAACGGCGG CCACGGCGGC GGTGCCACCG	1320
GCGGCGCCAG CGGCAAGGGC GGCAACGGCA CCAGCGGTGC CGCCAGCGGC TCAGGCGTCA	1380
TCAACGTCAC CGCCGGCCAC GGCGGCAACG GCGGCAATGG CCGCAACGGC GGCAACGGC	1439

(2) INFORMATION FOR SEQ ID NO:168:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 329 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:

GGGCCGGCGG GGCCGGATTT TCTCGTGCCT TGATTGTCGC TGGGGATAAC GGCGGTGATG	60
GTGGTAACGG CGGGATGGGC GGGGCTGGCG GGGCTGGCGG CCCC GGCGGG GCCGGCGGCC	120
TGATCAGCCT GCTGGGCGGC CAAGGCGCCG GCGGGGCCGG CGGGACCGGC GGGGCCGGCG	180
GTGTTGGCGG TGACGGCGGG GCCGGCGGCC CCGGCAACCA GGCCTTCAAC GCAGGTGCCG	240
GCGGGGCCGG CGGCCTGATC AGCCTGCTGG GCGGCCAAGG CGCCGGCGGG GCCGGCGGGA	300
CCGGCGGGGC CGGCGGTGTT GGCGGTGAC	329

(2) INFORMATION FOR SEQ ID NO:169:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 80 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:169:

GCAACGGTGG CAACGGCGGC ACCAGCACGA CCGTGGGGAT GGCCGGAGGT AACTGTGGTG	60
CCGCCGGGCT GATCGGCAAC	80

(2) INFORMATION FOR SEQ ID NO:170:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 392 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:

GGGCTGTGTC GCACTCACAC CGCCGCATTC GGCGACGTTG GCCGCCCAAT ATCCAGCTCA	60
AGGCCTACTA CTTACCGTCG GAGGACCGCC GCATCAAGGT GCGGGTCAGC GCCCAAGGAA	120
TCAAGGTCAT CGACCGCGAC GGGCATCGAG GCCGTCGTCG CGCGGCTCGG GCAGGATCCG	180

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CCCCGGCGCA CTTCGCGCGC CAAGCGGGCT CATCGCTCCG AACGGCGGCG ATCCTGTGAG	240
CACAACTGAT GGCGCGCAAC GAGATTCGTC CAATTGTCAA GCCGTGTTCG ACCGCAGGGA	300
CCGGTTATAC GTATGTCAAC CTATGTCACT CGCAAGAACC GGCATAACGA TCCCGTGATC	360
CGCCGACAGC CCACGAGTGC AAGACCGTTA CA	392

(2) INFORMATION FOR SEQ ID NO:171:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 535 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:171:

ACCGGCGCCA CCGGCGGCAC CGGGTTCGCC GGTGGCGCCG GCGGGGCCGG CGGGCAGGGC	60
GGTATCAGCG GTGCCGGCGG CACCAACGGC TCTGGTGGCG CTGGCGGCAC CGGCGGACAA	120
GGCGGCGCCG GGGGCGCTGG CGGGGCCGGC GCCGATAACC CCACCGGCAT CGGCGGCGCC	180
GGCGGCACCG GCGGCACCGG CGGAGCGGCC GGAGCCGGCG GGGCCGGTGG CGCCATCGGT	240
ACCGGCGGCA CCGGCGGCGC GGTGGGCAGC GTCGGTAACG CCGGGATCGG CGGTACCGGC	300
GGTACGGGTG GTGTCGGTGG TGCTGGTGGT GCAGGTGCGG CTGCGGCCGC TGGCAGCAGC	360
GCTACCGGTG GCGCCGGGTT CGCCGGCGGC GCCGGCGGAG AAGGCGGACC GGGCGGCAAC	420
AGCGGTGTGG GCGGCACCAA CGGCTCCGGC GCGCCGGCG GTGCAGGCGG CAAGGGCGGC	480
ACCGGAGGTG CCGGCGGGTC CGGCGCGGAC AACCCACCG GTGCTGGTTT CGCCG	535

(2) INFORMATION FOR SEQ ID NO:172:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 690 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:

CCGACGTCGC CGGGGCGATA CGGGGGTCAC CGACTACTAC ATCATCCGCA CCGAGAATCG	60
GCCGCTGCTG CAACCGCTGC GGGCGGTGCC GGTATCGGA GATCCGCTGG CCGACCTGAT	120
CCAGCCGAAC CTGAAGGTGA TCGTCAACCT GGGCTACGGC GACCCGAAC AC GGCTACTC	180
GACGAGCTAC GCCGATGTGC GAACGCCGTT CGGGCTGTGG CCGAACGTGC CGCCTCAGGT	240

CATCGCCGAT GCCCTGGCCG CCGGAACACA AGAAGGCATC CTTGACTTCA CGGCCGACCT	300
GCAGGCGCTG TCCGCGCAAC CGCTCACGCT CCCGCAGATC CAGCTGCCGC AACCCGCCGA	360
TCTGGTGGCC GCGGTGGCCG CCGCACCGAC GCCGGCCGAG GTGGTGAACA CGCTCGCCAG	420
GATCATCTCA ACCAACTACG CCGTCCTGCT GCCCACCCTG GACATCGCCC TCGCCTGGTC	480
ACCACCCTGC CGCTGTACAC CACCCAACTG TTCGTCAGGC AACTCGCTGC GGGCAATCTG	540
ATCAACGCGA TCGGCTATCC CCTGGCGGCC ACCGTAGGTT TAGGCACGAT CGATAGCGGG	600
CGGCGTGGAA TTGCTACCC TCCTCGCGGC GGCTCGGAC ACCGTTCGAA ACATCGAGGG	660
CCTCGTCACC TAACGGATTC CCGACGGCAT	690

(2) INFORMATION FOR SEQ ID NO:173:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 407 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:173:

ACGGTGACGG CGGTACTGGC GGCGGCCACG GCGGCAACGG CGGGAATCCC GGGTGGCTCT	60
TGGGCACAGC CGGGGGTGGC GGCAACGGTG GCGCCGGCAG CACCGGTACT GCAGGTGGCG	120
GCTCTGGGGG CACCGGCGGC GACGGCGGGA CCGGCGGGCG TGGCGGCCTG TTAATGGGCG	180
CCGGCGCCGG CGGGCACGGT GGCACCTGGCG GCGCGGGCGG TGCCGGTGTC GACGGTGGCG	240
GCGCCGGCGG GGCCGGCGGG GCCGGCGGCA ACGGCGGCGC CGGGGGTCAA GCCGCCCTGC	300
TGTTGCGGGC CGGCGGCACC GGCGGAGCCG GCGGCTACGG CGGCGATGGC GGTGGCGGCG	360
GTGACGGCTT CGACGGCACG ATGGCCGGCC TGGGTGGTAC CGGTGGC	407

(2) INFORMATION FOR SEQ ID NO:174:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 468 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:

GATCGGTCAG CGCATCGCCC TCGGCGGCAA GCGATTCCGC GGTCTCACCG AAGAACATCG	60
TGCACGCGGC GGCGCGGACC AGCCCGCTGC GCTGCGGCGC GTCGAACGCC TCCAGCAGGC	120

ACAGCCAGTC CTTGGCGGCC TGCAGGGCGA ACACGTCGGT GTCACCGGTG TAGATCGCCG	180
GGATGCCCCG CTCCGCCAAC GCATTCCGGC ACGCCCGCGC GTCTTTGTGA TGCTCGACGA	240
TCACCGCGAT GTCTGCGGCC ACCACGGGCC GCCCGGCGAA GGTGGCCCCG CTGGCCAGTA	300
GCGCCGCGAC GTCGGCGGCC AGGTCGTCGG GGATGTGCCG GCGCAGCGCT CCGGCGCGAC	360
GCCCGAAAAA CGACCCCTCA CCCAGCTGGG TCCCGCTGGC ATATCCCTTG CCGTCCTGGG	420
CGATATTGGA CGCGCATGCC CCGACCGCGT ACAGGCCGGC CACCACCG	468

(2) INFORMATION FOR SEQ ID NO:175:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 219 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:175:

GGTGGTAACG GCGGCCAGGG TGGCATCGGC GGCGCCGGCG AGAGAGGCGC CGACGGCGCC	60
GGCCCCAATG CTAACGGCGC AAACGGCGAG AACGGCGGTA GCGGTGGTAA CGGTGGCGAC	120
GGCGGCGCCG GCGGCAATGG CGGCGCGGGC GGCAACGCGC AGGCGGCCGG GTACACCGAC	180
GGCGCCACGG GCACCGGCGG CGACGGCGGC AACGGCGGC	219

(2) INFORMATION FOR SEQ ID NO:176:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 494 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:

TAGTCCGGC GAGGGCGGCA AGGGCGGCGA CGGTGGCCAC GGCGGTGACG GCGTCGGCGG	60
CAACAGTTCC GTCACCCAAG GCGGCAGCGG CGGTGGCGGC GGCGCCGGCG GCGCCGGCGG	120
CAGCGGCTTT TTCGGCGGCA AGGGCGGCTT CGGCGGCGAC GGCGGTCAGG GCGGCCCCAA	180
CGGCGGCGGT ACCGTCGGCA CCGTGGCCGG TGGCGGCGGC AACGGCGGTG TCGGCGGCCG	240
GGGCGGCGAC GGCGTCTTTG CCGGTGCCGG CGGCCAGGGC GGCCTCGGTG GGCAGGGCGG	300
CAATGGCGGC GGCTCCACCG GCGGCAACGG CGGCCTTGGC GGCGCGGGCG GTGGCGGAGG	360
CAACGCCCCG GCTCGTGCCG AATCCGGGCT GACCATGGAC AGCGCGGCCA AGTTCGCTGC	420

CATCGCATCA GGCGCGTACT GCCCCGAACA CCTGGAACAT CACCCGAGTT AGCGGGGCGC 480
ATTTCCTGAT CACC 494

(2) INFORMATION FOR SEQ ID NO:177:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 220 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:177:

GGGCCGGTGG TGCCGCGGGC CAGCTCTTCA GCGCCGAGG CGCGGCGGGT GCCGTTGGGG 60
TTGGCGGCAC CGGCGGCCAG GGTGGGGCTG GCGGTGCCGG AGCGGCCGGC GCCGACGCCC 120
CCGCCAGCAC AGGTCTAACC GGTGGTACCG GGTTCGCTGG CGGGGCCGGC GGCCTCGGCG 180
GCCAGAGCGG CAACGCCATT GCCGGCGGCA TCAACGGCTC 220

(2) INFORMATION FOR SEQ ID NO:178:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 388 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:178:

ATGGCGGCAA CGGGGGCCCC GGCGGTGCTG GCGGGGCCGG CGACTACAAT TTCCAACGGC 60
GGGCAGGGTG GTGCCGGCGG CCAAGGCGGC CAAGGCGGCC TGGGCGGGGC AAGCACCACC 120
TGATCGGCCT AGCCGCACCC GGGAAAGCCG ATCCAACAGG CGACGATGCC GCCTTCCTTG 180
CCGCGTTGGA CCAGGCCGGC ATCACCTACG CTGACCCAGG CCACGCCATA ACGGCCGCCA 240
AGGCGATGTG TGGGCTGTGT GCTAACGGCG TAACAGGTCT ACAGCTGGTC GCGGACCTGC 300
GGGACTACAA TCCCGGGCTG ACCATGGACA GCGCGGCCAA GTTCGCTGCC ATCGCATCAG 360
GCGCGTACTG CCCC GAACAC CTGGAACA 388

(2) INFORMATION FOR SEQ ID NO:179:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:179:

GCAAAGGCGG CACCGGCGGG GCCGGCATGA ACAGCCTCGA CCCGCTGCTA GCCGCCCAAG	60
ACGGCGGCCA AGGCGGCACC GGCGGCACCG GCGGCAACGC CGGCGCCGGC GGCACCAGCT	120
TCACCCAAGG CGCCGACGGC AACGCCGGCA ACGGCGGTGA CGGCGGGGTC GGCGGCAACG	180
GCGGAAACGG CGGAAACGGC GCAGACAACA CCACCACCGC CGCCGCCGGC ACCACAGGCG	240
GCGACGGCGG GGCCGGCGGG GCCGGCGGAA CCGGCGGAAC CGGCGGAGCC GCCGGCACCG	300
GCACCGGCGG CCAACAAGGC AACGGCGGCA ACGGCGGCAC CGGCGGCAAA GGCGGCACCG	360
GCGGCGACGG TGCACTCTCA GGCAGCACCG GTGGTGCCGG	400

(2) INFORMATION FOR SEQ ID NO:180:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 538 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:

GGCAACGGCG GCAACGGCGG CATCGCCGGC ATTGGGCGGC AACGGCGTTC CGGGACGGGC	60
AGCGGCAACG GCGGCCAACG GCGGCAGCGG CGGCAACGGC GGCAACGCCG GCATGGGCGG	120
CAACAGCGGC ACCGGCAGCG GCGACGGCGG TGCCGGCGGG AACGGCGGCG CGGCGGGCAC	180
GGGCGGCACC GGCGGCGACG GCGGCCTCAC CGGTACTGGC GGCACCGGCG GCAGCGGTGG	240
CACCGGCGGT GACGGCGGTA ACGGCGGCAA CGGAGCAGAT AACACCGCAA ACATGACTGC	300
GCAGGCGGGC GGTGACGGTG GCAACGGCGG CGACGGTGGC TTCGGCGGCG GGGCCGGGGC	360
CGGCGGCGGT GGCTTGACCG CTGGCGCCAA CGGCACCGGC GGGCAAGGCG GCGCCGGCGG	420
CGATGGCGGC AACGGGGCCA TCGGCGGCCA CGGCCCACTC ACTGACGACC CCGGCGGCAA	480
CGGGGGCACC GGCGGCAACG GCGGCACCGG CGGCACCGGC GGCGCGGGCA TCGGCAGC	538

(2) INFORMATION FOR SEQ ID NO:181:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 239 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:181:

GGGCCGGTGG TGCCGCGGGC CAGCTCTTCA GCGCCGGAGG CGCGGCGGGT GCCGTTGGGG	60
TTGGCGGCAC CGGCGGCCAG GGTGGGGCTG GCGGTGCCGG AGCGGCCGGC GCCGACGCCC	120
CCGCCAGCAC AGGTCTAACC GGTGGTACCG GGTTCGCTGG CGGGGCCGGC GGCCTCGGCG	180
GCCACGGCGG CAACGCCATT GCCGGCGGCA TCAACGGCTC CGGTGGTGCC GGCGGCACC	239

(2) INFORMATION FOR SEQ ID NO:182:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 985 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:182:

AGCAGCGCTA CCGGTGGCGC CGGGTTCGCC GCGGCGCCCG GCGGAGAAGG CGGAGCGGGC	60
GGCAACAGCG GTGTGGGCGG CACCAACGGC TCCGGCGGCG CCGGCGGTGC AGGCGGCAAG	120
GGCGGCACCG GAGGTGCCGG CGGGTCCGGC GCGGACAACC CCACCGGTGC TGGTTTCGCC	180
GGTGGCGCCG GCGGCACAGG TGGCGCGGCC GCGGCCGGCG GGGCCGGCGG GGCACCGGT	240
ACCGGCGGCA CCGGCGGCGT TGTCGGCGCC ACCGGTAGTG CAGGCATCGG CGGGGCCGGC	300
GGCCGCGGCG GTGACGGCGG CGATGGGGCC AGCGGTCTCG GCCTGGGCCT CTCCGGCTTT	360
GACGGCGGCC AAGGCGGCCA AGGCGGGGCC GCGGCAGCG CCGGCGCCGG CGGCATCAAC	420
GGGGCCGGCG GGGCCGGCGG CAACGGCGGC GACGGCGGGG ACGGCGCAAC CGGTGCCGCA	480
GGTCTCGGCG ACAACGGCGG GGTCCGGGT GACGGTGGGG CCGGTGGCGC CGCCGGCAAC	540
GGCGGCAACG CGGGCGTCGG CCTGACAGCC AAGGCCGGCG ACGGCGGCGC CGCGGGCAAT	600
GGCGGCAACG GGGGCGCCGG CGGTGCTGGC GGGGCGGGCG ACAACAATTT CAACGGCGGC	660
CAGGGTGGTG CCGGCGGCCA AGGCGGCCAA GCGGCTTG GCGGGCAAG CACCACCTGA	720
TCGGCCTAGC CGCACCCGGG AAAGCCGATC CAACAGGCGA CGATGCCGCC TTCCTTGCCG	780
CGTTGGACCA GGCCGGCATC ACCTACGCTG ACCCAGGCCA CGCCATAACG GCCGCCAAGG	840
CGATGTGTGG GCTGTGTGCT AACGGCGTAA CAGGTCTACA GCTGGTCGCG GACCTGCGGG	900
AATACAATCC CGGGCTGACC ATGGACAGCG CGGCCAAGTT CGCTGCCATC GCATCAGGCG	960
CGTACTGCCC CGAACACCTG GAACA	985

(2) INFORMATION FOR SEQ ID NO:183:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2138 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:183:

CGGCACGAGG ATCGGTACCC CGCGGCATCG GCAGCTGCCG ATTCGCCGGG TTTCCCCACC	60
CGAGGAAAGC CGCTACCAGA TGGCGCTGCC GAAGTAGGGC GATCCGTTCG CGATGCCGGC	120
ATGAACGGGC GGCATCAAAT TAGTGCAGGA ACCTTTCAGT TTAGCGACGA TAATGGCTAT	180
AGCACTAAGG AGGATGATCC GATATGACGC AGTCGCAGAC CGTGACGGTG GATCAGCAAG	240
AGATTTTGA CAGGGCCAAC GAGGTGGAGG CCCCAGATGGC GGACCCACCG ACTGATGTCC	300
CCATCACACC GTGCGAACTC ACGGCGGCTA AAAACGCCGC CCAACAGCTG GTATTGTCCG	360
CCGACAACAT GCGGGAATAC CTGGCGGCCG GTGCCAAGA GCGGCAGCGT CTGGCGACCT	420
CGCTGCGCAA CGCGGCCAAG GCGTATGGCG AGGTTGATGA GGAGGCTGCG ACCGCGCTGG	480
ACAACGACGG CGAAGGAACT GTGCAGGCAG AATCGGCCGG GGCCGTCGGA GGGGACAGTT	540
CGGCCGAACT AACCGATACG CCGAGGGTGG CCACGGCCGG TGAACCCAAC TTCATGGATC	600
TCAAAGAAGC GGCAAGGAAG CTCGAAACGG GCGACCAAGG CGCATCGCTC GCGCACTTTG	660
CGGATGGGTG GAACACTTTC AACCTGACGC TGCAAGGCGA CGTCAAGCGG TTCCGGGGGT	720
TTGACAACCTG GGAAGGCGAT GCGGCTACCG CTTGCGAGGC TTCGCTCGAT CAACAACGGC	780
AATGGATACT CCACATGGCC AAATTGAGCG CTGCGATGGC CAAGCAGGCT CAATATGTCG	840
CGCAGCTGCA CGTGTGGGCT AGGCGGGAAC ATCCGACTTA TGAAGACATA GTCGGGCTCG	900
AACGGCTTTA CGCGGAAAAC CCTTCGGCCC GCGACCAAAT TCTCCCGGTG TACGCGGAGT	960
ATCAGCAGAG GTCGGAGAAG GTGCTGACCG AATACAACAA CAAGGCAGCC CTGGAACCGG	1020
TAAACCCGCC GAAGCCTCCC CCCGCCATCA AGATCGACCC GCCCCGCCT CCGCAAGAGC	1080
AGGGATTGAT CCCTGGCTTC CTGATGCCGC CGTCTGACGG CTCCGGTGTG ACTCCCGGTA	1140
CCGGGATGCC AGCCGCACCG ATGGTTCCGC CTACCGGATC GCCGGGTGGT GGCCTCCCGG	1200
CTGACACGGC GGCGCAGCTG ACGTCGGCTG GCGGGAAGC CGCAGCGCTG TCGGGCGACG	1260
TGGCGGTCAA AGCGGCATCG CTCGGTGGCG GTGGAGGCGG CGGGGTGCCG TCGGCGCCGT	1320
TGGGATCCGC GATCGGGGGC GCCGAATCGG TGCGGCCCCG TGGCGCTGGT GACATTGCCG	1380
GCTTAGGCCA GGGAAGGGCC GCGGCGGGCG CCGCGCTGGG CGGCGGTGGC ATGGGAATGC	1440
CGATGGGTGC CGCGCATCAG GGACAAGGGG GCGCCAAGTC CAAGGGTTCT CAGCAGGAAG	1500

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ACGAGGCGCT CTACACCGAG GATCGGGCAT GGACCGAGGC CGTCATTGGT AACCGTCGGC      1560
GCCAGGACAG TAAGGAGTCG AAGTGAGCAT GGACGAATTG GACCCGCATG TCGCCCGGGC      1620
GTTGACGCTG GCGGCGCGGT TTCAGTCGGC CCTAGACGGG ACGCTCAATC AGATGAACAA      1680
CGGATCCTTC CGCGCCACCG ACGAAGCCGA GACCGTCGAA GTGACGATCA ATGGGCACCA      1740
GTGGCTCACC GGCCTGCGCA TCGAAGATGG TTTGCTGAAG AAGCTGGGTG CCGAGGCGGT      1800
GGCTCAGCGG GTCAACGAGG CGCTGCACAA TGCGCAGGCC GCGGCGTCCG CGTATAACGA      1860
CGCGGCGGGC GAGCAGCTGA CCGCTGCGTT ATCGGCCATG TCCCGCGCGA TGAACGAAGG      1920
AATGGCCTAA GCCCATTGTT GCGGTGGTAG CGACTACGCA CCGAATGAGC GCCGCAATGC      1980
GGTCATT CAG CGCGCCCGAC ACGGCGTGAG TACGCATTGT CAATGTTTTG ACATGGATCG      2040
GCCGGGTTCG GAGGGCGCCA TAGTCCTGGT CGCCAATATT GCCGCAGCTA GCTGGTCTTA      2100
GGTTCGGTTA CGCTGGTTAA TTATGACGTC CGTTACCA                                2138

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(2) INFORMATION FOR SEQ ID NO:184:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 460 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:

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Met Thr Gln Ser Gln Thr Val Thr Val Asp Gln Gln Glu Ile Leu Asn
1          5          10          15
Arg Ala Asn Glu Val Glu Ala Pro Met Ala Asp Pro Pro Thr Asp Val
20        25        30
Pro Ile Thr Pro Cys Glu Leu Thr Ala Ala Lys Asn Ala Ala Gln Gln
35        40        45
Leu Val Leu Ser Ala Asp Asn Met Arg Glu Tyr Leu Ala Ala Gly Ala
50        55        60
Lys Glu Arg Gln Arg Leu Ala Thr Ser Leu Arg Asn Ala Ala Lys Ala
65        70        75        80
Tyr Gly Glu Val Asp Glu Glu Ala Ala Thr Ala Leu Asp Asn Asp Gly
85        90        95
Glu Gly Thr Val Gln Ala Glu Ser Ala Gly Ala Val Gly Gly Asp Ser
100       105       110
Ser Ala Glu Leu Thr Asp Thr Pro Arg Val Ala Thr Ala Gly Glu Pro
115       120       125
Asn Phe Met Asp Leu Lys Glu Ala Ala Arg Lys Leu Glu Thr Gly Asp
130       135       140

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179

Gln Gly Ala Ser Leu Ala His Phe Ala Asp Gly Trp Asn Thr Phe Asn
 145 150 155 160
 Leu Thr Leu Gln Gly Asp Val Lys Arg Phe Arg Gly Phe Asp Asn Trp
 165 170 175
 Glu Gly Asp Ala Ala Thr Ala Cys Glu Ala Ser Leu Asp Gln Gln Arg
 180 185 190
 Gln Trp Ile Leu His Met Ala Lys Leu Ser Ala Ala Met Ala Lys Gln
 195 200 205
 Ala Gln Tyr Val Ala Gln Leu His Val Trp Ala Arg Arg Glu His Pro
 210 215 220
 Thr Tyr Glu Asp Ile Val Gly Leu Glu Arg Leu Tyr Ala Glu Asn Pro
 225 230 235 240
 Ser Ala Arg Asp Gln Ile Leu Pro Val Tyr Ala Glu Tyr Gln Gln Arg
 245 250 255
 Ser Glu Lys Val Leu Thr Glu Tyr Asn Asn Lys Ala Ala Leu Glu Pro
 260 265 270
 Val Asn Pro Pro Lys Pro Pro Pro Ala Ile Lys Ile Asp Pro Pro Pro
 275 280 285
 Pro Pro Gln Glu Gln Gly Leu Ile Pro Gly Phe Leu Met Pro Pro Ser
 290 295 300
 Asp Gly Ser Gly Val Thr Pro Gly Thr Gly Met Pro Ala Ala Pro Met
 305 310 315 320
 Val Pro Pro Thr Gly Ser Pro Gly Gly Gly Leu Pro Ala Asp Thr Ala
 325 330 335
 Ala Gln Leu Thr Ser Ala Gly Arg Glu Ala Ala Ala Leu Ser Gly Asp
 340 345 350
 Val Ala Val Lys Ala Ala Ser Leu Gly Gly Gly Gly Gly Gly Gly Val
 355 360 365
 Pro Ser Ala Pro Leu Gly Ser Ala Ile Gly Gly Ala Glu Ser Val Arg
 370 375 380
 Pro Ala Gly Ala Gly Asp Ile Ala Gly Leu Gly Gln Gly Arg Ala Gly
 385 390 395 400
 Gly Gly Ala Ala Leu Gly Gly Gly Gly Met Gly Met Pro Met Gly Ala
 405 410 415
 Ala His Gln Gly Gln Gly Gly Ala Lys Ser Lys Gly Ser Gln Gln Glu
 420 425 430
 Asp Glu Ala Leu Tyr Thr Glu Asp Arg Ala Trp Thr Glu Ala Val Ile
 435 440 445
 Gly Asn Arg Arg Arg Gln Asp Ser Lys Glu Ser Lys
 450 455 460

(2) INFORMATION FOR SEQ ID NO:185:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 277 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:185:

Ala Gly Asn Val Thr Ser Ala Ser Gly Pro His Arg Phe Gly Ala Pro
 1 5 10 15
 Asp Arg Gly Ser Gln Arg Arg Arg Arg His Pro Ala Ala Ser Thr Ala
 20 25 30
 Thr Glu Arg Cys Arg Phe Asp Arg His Val Ala Arg Gln Arg Cys Gly
 35 40 45
 Phe Pro Pro Ser Arg Arg Gln Leu Arg Arg Arg Val Ser Arg Glu Ala
 50 55 60
 Thr Thr Arg Arg Ser Gly Arg Arg Asn His Arg Cys Gly Trp His Pro
 65 70 75 80
 Gly Thr Gly Ser His Thr Gly Ala Val Arg Arg Arg His Gln Glu Ala
 85 90 95
 Arg Asp Gln Ser Leu Leu Leu Arg Arg Arg Gly Arg Val Asp Leu Asp
 100 105 110
 Gly Gly Gly Arg Leu Arg Arg Val Tyr Arg Phe Gln Gly Cys Leu Val
 115 120 125
 Val Val Phe Gly Gln His Leu Leu Arg Pro Leu Leu Ile Leu Arg Val
 130 135 140
 His Arg Glu Asn Leu Val Ala Gly Arg Arg Val Phe Arg Val Lys Pro
 145 150 155 160
 Phe Glu Pro Asp Tyr Val Phe Ile Ser Arg Met Phe Pro Pro Ser Pro
 165 170 175
 His Val Gln Leu Arg Asp Ile Leu Ser Leu Leu Gly His Arg Ser Ala
 180 185 190
 Gln Phe Gly His Val Glu Tyr Pro Leu Pro Leu Leu Ile Glu Arg Ser
 195 200 205
 Leu Ala Ser Gly Ser Arg Ile Ala Phe Pro Val Val Lys Pro Pro Glu
 210 215 220
 Pro Leu Asp Val Ala Leu Gln Arg Gln Val Glu Ser Val Pro Pro Ile
 225 230 235 240
 Arg Lys Val Arg Glu Arg Cys Ala Leu Val Ala Arg Phe Glu Leu Pro
 245 250 255
 Cys Arg Phe Phe Glu Ile His Glu Val Gly Phe Thr Gly Arg Gly His

181

260 265 270

Pro Arg Arg Ile Gly
275

(2) INFORMATION FOR SEQ ID NO:186:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 192 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:186:

Arg	Val	Ala	Ala	Ser	Phe	Ile	Asp	Trp	Leu	Asp	Ser	Pro	Asp	Ser	Pro	1	5	10	15
Leu	Asp	Pro	Ser	Leu	Val	Ser	Ser	Leu	Leu	Asn	Ala	Val	Ser	Cys	Gly	20	25	30	
Ala	Glu	Ser	Ser	Ala	Ser	Ser	Ser	Ala	Arg	Ser	Gly	Asn	Gly	Ser	Arg	35	40	45	
Trp	Thr	Ser	Met	Pro	Ser	Gly	Thr	Arg	Pro	Gly	Pro	Arg	Arg	Ala	Thr	50	55	60	
Ser	Arg	Asp	Asp	Arg	Arg	Ser	Ala	Thr	Ser	Val	Ile	Pro	Ser	Arg	Arg	65	70	75	80
Ser	Val	Ala	Pro	Arg	Ala	Glu	Phe	Gly	Thr	Arg	Leu	Ala	Ser	His	Arg	85	90	95	
Ala	Ser	Pro	Ser	Asn	Ala	Cys	Pro	Val	Arg	Ile	Val	Thr	Ser	Ala	Ser	100	105	110	
Gly	Arg	Pro	Ile	Ser	Ser	Pro	Pro	Ile	Val	Arg	Ser	Arg	Ser	Cys	Val	115	120	125	
Asp	Lys	Asn	Gly	Arg	Arg	Cys	Ala	Ser	Gly	Tyr	Arg	Arg	Leu	Asn	Arg	130	135	140	
Ala	Arg	Ser	Ser	Ser	Ile	Ala	Ala	Arg	Cys	Arg	Thr	Ile	Gly	Thr	Phe	145	150	155	160
Arg	Arg	Ser	Arg	Tyr	Ser	Ala	Ser	Met	Arg	Val	Ser	Thr	Asn	Ser	Pro	165	170	175	
His	Val	Thr	His	Gly	Val	Ala	Pro	Gly	Val	Thr	Arg	Arg	Ile	Gly	Gly	180	185	190	

(2) INFORMATION FOR SEQ ID NO:187:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 196 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:

182

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:187:

Gln	Glu	Arg	Pro	Gln	Met	Cys	Gln	Arg	Val	Ser	Glu	Ile	Glu	Pro	Arg	1	5	10	15
Thr	Gln	Phe	Phe	Asn	Arg	Cys	Ala	Leu	Pro	His	Tyr	Trp	His	Phe	Pro	20	25	30	
Ala	Val	Ala	Val	Phe	Ser	Lys	His	Ala	Ser	Leu	Asp	Glu	Leu	Ala	Pro	35	40	45	
Arg	Asn	Pro	Arg	Arg	Ser	Ser	Arg	Arg	Asp	Ala	Glu	Asp	Arg	Arg	Val	50	55	60	
Ile	Phe	Ala	Ala	Thr	Leu	Val	Ala	Val	Asp	Pro	Pro	Leu	Arg	Gly	Ala	65	70	75	80
Gly	Gly	Glu	Ala	Asp	Gln	Leu	Ile	Asp	Leu	Gly	Val	Cys	Arg	Arg	Gln	85	90	95	
Ala	Gly	Arg	Val	Arg	Arg	Gly	Gln	Glu	Leu	His	His	Arg	His	Arg	His	100	105	110	
Gln	Gly	Ala	Ala	Pro	Asp	Leu	Arg	Arg	Arg	Arg	Arg	His	Arg	Arg	Val	115	120	125	
Gln	Gln	His	Arg	Arg	Leu	Gln	Arg	Val	Arg	Gln	Leu	Arg	Arg	Tyr	Val	130	135	140	
Gln	Thr	Ala	His	His	Arg	Arg	Phe	Ala	Arg	Thr	Asp	Arg	Val	Arg	His	145	150	155	160
His	Val	Arg	Gly	Pro	Ser	Asn	His	Arg	Arg	Arg	Arg	Val	Tyr	Arg	Gly	165	170	175	
Arg	His	Ser	Gly	Ala	Gly	Gly	Cys	Pro	Ala	Gly	Gly	Ala	Gly	Ser	Val	180	185	190	
Gly	Gly	Ser	Ala													195			

(2) INFORMATION FOR SEQ ID NO:188:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 311 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:188:

Val Arg Cys Gly Thr Leu Val Pro Val Pro Met Val Glu Phe Leu Thr

183

1	5	10	15
Ser Thr Asn Ala Pro Ser Leu Pro Ser Ala Tyr Ala Glu Val Asp Lys	20	25	30
Leu Ile Gly Leu Pro Ala Gly Thr Ala Lys Arg Trp Ile Asn Gly Tyr	35	40	45
Glu Arg Gly Gly Lys Asp His Pro Pro Ile Leu Arg Val Thr Pro Gly	50	55	60
Ala Thr Pro Trp Val Thr Trp Gly Glu Phe Val Glu Thr Arg Met Leu	65	70	75
Ala Glu Tyr Arg Asp Arg Arg Lys Val Pro Ile Val Arg Gln Arg Ala	85	90	95
Ala Ile Glu Glu Leu Arg Ala Arg Phe Asn Leu Arg Tyr Pro Leu Ala	100	105	110
His Leu Arg Pro Phe Leu Ser Thr His Glu Arg Asp Leu Thr Met Gly	115	120	125
Gly Glu Glu Ile Gly Leu Pro Asp Ala Glu Val Thr Ile Arg Thr Gly	130	135	140
Gln Ala Leu Leu Gly Asp Ala Arg Trp Leu Ala Ser Leu Val Pro Asn	145	150	155
Ser Ala Arg Gly Ala Thr Leu Arg Arg Leu Gly Ile Thr Asp Val Ala	165	170	175
Asp Leu Arg Ser Ser Arg Glu Val Ala Arg Arg Gly Pro Gly Arg Val	180	185	190
Pro Asp Gly Ile Asp Val His Leu Leu Pro Phe Pro Asp Leu Ala Asp	195	200	205
Asp Asp Ala Asp Asp Ser Ala Pro His Glu Thr Ala Phe Lys Arg Leu	210	215	220
Leu Thr Asn Asp Gly Ser Asn Gly Glu Ser Gly Glu Ser Ser Gln Ser	225	230	235
Ile Asn Asp Ala Ala Thr Arg Tyr Met Thr Asp Glu Tyr Arg Gln Phe	245	250	255
Pro Thr Arg Asn Gly Ala Gln Arg Ala Leu His Arg Val Val Thr Leu	260	265	270
Leu Ala Ala Gly Arg Pro Val Leu Thr His Cys Phe Ala Gly Lys Asp	275	280	285
Arg Thr Gly Phe Val Val Ala Leu Val Leu Glu Ala Val Gly Leu Asp	290	295	300
Arg Asp Val Ile Val Ala Asp	305	310	

(2) INFORMATION FOR SEQ ID NO:189:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2072 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:189:

CTCGTGCCGA TTCGGCACGA GCTGAGCAGC CCAAGGGGCC GTTCGGCGAA GTCATCGAGG	60
CATTCGCCGA CGGGCTGGCC GGCAAGGGTA AGCAAATCAA CACCACGCTG AACAGCCTGT	120
CGCAGGCGTT GAACGCCTTG AATGAGGGCC GCGGCGACTT CTTCGCGGTG GTACGCAGCC	180
TGGCGCTATT CGTCAACGCG CTACATCAGG ACGACCAACA GTTCGTCGCG TTGAACAAGA	240
ACCTTGCGGA GTTCACCGAC AGGTTGACCC ACTCCGATGC GGACCTGTCG AACGCCATCC	300
AGCAATTCGA CAGCTTGCTC GCCGTCGCGC GCCCCTTCTT CGCCAAGAAC CGCGAGGTGC	360
TGACGCATGA CGTCAATAAT CTCGCGACCG TGACCACCAC GTTGCTGCAG CCCGATCCGT	420
TGGATGGGTT GGAGACCGTC CTGCACATCT TCCGACGCT GCGGCGGAAC ATTAACCAGC	480
TTTACCATCC GACACACGGT GGCGTGGTGT CGCTTTCGCG GTTCACGAAT TTCGCCAACC	540
CGATGGAGTT CATCTGCAGC TCGATTGAGG CGGGTAGCCG GCTCGGTTAT CAAGAGTCGG	600
CCGAAGTCTG TGCAGAGTAT CTGGCGCCAG TCCTCGATGC GATCAAGTTC AACTACTTTC	660
CGTTCGGCCT GAACGTGGCC AGCACCGCCT CGACACTGCC TAAAGAGATC GCGTACTCCG	720
AGCCCCGCTT GCAGCCGCCC AACGGGTACA AGGACACCAC GGTGCCCCGGC ATCTGGGTGC	780
CGGATACGCC GTTGTCACAC CGCAACACGC AGCCCGGTTG GGTGGTGGCA CCCGGGATGC	840
AAGGGGTTC AAGTGGGACCG ATCACGCAGG GTTTGCTGAC GCCGGAGTCC CTGGCCGAAC	900
TCATGGGTGG TCCCGATATC GCCCCTCCGT CGTCAGGGCT GCAAACCCCG CCCGGACCCC	960
CGAATGCGTA CGACGAGTAC CCCGTGCTGC CGCCGATCGG TTTACAGGCC CCACAGGTGC	1020
CGATACCACC GCCGCCTCCT GGGCCCGACG TAATCCCGGG TCCGGTGCCA CCGGTCTTGG	1080
CGGCGATCGT GTTCCCAAGA GATCGCCCGG CAGCGTCGGA AACTTCGAC TACATGGGCC	1140
TCTTGTTGCT GTCGCCGGGC CTGGCGACCT TCCTGTTTCGG GGTGTCATCT AGCCCCGCCC	1200
GTGGAACGAT GGCCGATCGG CACGTGTTGA TACCGGCGAT CACCGGCCTG GCGTTGATCG	1260
CGGCATTCTG CGCACATTCG TGGTACCGCA CAGAACATCC GCTCATAGAC ATGCGCTTGT	1320
TCCAGAACCG AGCGGTCGCG CAGGCCAACA TGACGATGAC GGTGCTCTCC CTCGGGCTGT	1380
TTGGCTCCTT CTTGCTGCTC CCGAGCTACC TCCAGCAAGT GTTGACCAA TCACCGATGC	1440
AATCGGGGGT GCATATCATC CCACAGGGCC TCGGTGCCAT GCTGGCGATG CCGATCGCCG	1500
GAGCGATGAT GGACCGACCG GGACCGGCCA AGATCGTGCT GGTGGGATC ATGCTGATCG	1560

CTGCGGGGTT	GGGCACCTTC	GCCTTTGGTG	TCGCGCGGCA	AGCGGACTAC	TTACCCATTC	1620
TGCCGACCGG	GCTGGCAATC	ATGGGCATGG	GCATGGGCTG	CTCCATGATG	CCACTGTCCG	1680
GGGCGGCAGT	GCAGACCCTG	GCCCCACATC	AGATCGCTCG	CGGTTTCGACG	CTGATCAGCG	1740
TCAACCAGCA	GGTGGGCGGT	TCGATAGGGA	CCGCACTGAT	GTCGGTGCTG	CTCACCTACC	1800
AGTTCAATCA	CAGCGAAATC	ATCGCTACTG	CAAAGAAAGT	CGCACTGACC	CCAGAGAGTG	1860
GCGCCGGGCG	GGGGGCGGCG	GTTGACCCTT	CCTCGCTACC	GCGCCAAACC	AACTTCGCGG	1920
CCCAACTGCT	GCATGACCTT	TCGCACGCCT	ACGCGGTGGT	ATTCTGTGATA	GCGACCGCGC	1980
TAGTGGTCTC	GACGCTGATC	CCCGCGGCAT	TCCTGCCGAA	ACAGCAGGCT	AGTCATCGAA	2040
GAGCACCGTT	GCTATCCGCA	TGACGTCTGC	TT			2072

(2) INFORMATION FOR SEQ ID NO:190:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1923 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:190:

TCACCCCGGA	GAAGTCGTT	GTCGACGACC	TGGACATCGA	CTCGCTGTCG	ATGGTCGAGA	60
TCGCCGTGCA	GACCGAGGAC	AAGTACGGCG	TCAAGATCCC	CGACGAGGAC	CTCGCCGGTC	120
TGCGTACCGT	CGGTGACGTT	GTCGCCTACA	TCCAGAAGCT	CGAGGAAGAA	AACCCGGAGG	180
CGGCTCAGGC	GTTGCGCGCG	AAGATTGAGT	CGGAGAACCC	CGATGCGGCA	CGAGCAGATC	240
GGTGCGTTTC	ACCCACATCG	CAAGCTCGAG	ACGCCCGTCG	TCCTCTTGCA	CGCTCAGCCA	300
GGTTGGCGTG	TCGCCGCCTT	CCAGCAAGTG	TTCCCAACCAC	ACGAAGGGAC	CCTCGCGAAA	360
GGTGACTGAT	CCGCGGACCA	CATAGTCGAT	GCCACCGTGG	CTGACAATTG	CGCCGGGTCC	420
GAGTTGGCGG	GGGCCGAATT	GCGGCATTGC	GTCGAAGGCC	AGCGGATCCC	GGCGCCCGCC	480
CGGCGTGGCT	GGTGTTTTGG	GCCGCCGGAT	GGCCACGACG	AGAACGACGA	TGGCGGCGAT	540
GAACAGCGCC	ACGGCAATCA	CGACCAGCAG	ATTTCCACG	CATACCTCT	CGTACCGCTG	600
CGCCGCGGTT	GGTCGATCGG	TCGCATATCG	ATGGCGCCGT	TTAACGTAAC	AGCTTTCGCG	660
GGACCGGGGG	TCACAACGGG	CGAGTTGTCC	GGCCGGGAAC	CCGGCAGGTC	TCGGCCGCGG	720
TCACCCAGC	TCACTGGTGC	ACCATCCGGG	TGTCGGTGAG	CGTGCAACTC	AAACACACTC	780
AACGGCAACG	GTTTCTCAGG	TCACCAGCTC	AACCTCGACC	CGCAATCGCT	CGTACGTTTC	840
GACCGCGCGC	AGGTCGCGAG	TCAGCAGCTT	TGCGCCGGCA	GCTTTCGCCG	TGAAGCCGAC	900

CAGGGCATCG TAGGTTGCGC CACCGGTGAC ATCGTGCTCG GCGAGGTGGT CGGTCAAGCC	960
GCGATATGAG CAGGCATCCA GTGCCAGGTA GTTGCTGGAG GTGATGTCCG CCAAGTAGGC	1020
GTGGACGGCA ACAGGGGCAA TACGATGCGG CGGTGGTAGC CGGGTCAAGA CCGAATAGGT	1080
TTCCACAGCC GCGTGCGCGA TCAGATGGAC GCCACGGTTG AGCGCGCGCA CGGCGGCCTC	1140
GTGCCCTTCG TGCCAGGTCG CGAATCCGGC AACCAGCACG CTGGTGTCTG GTGCGATCAC	1200
CGCCGTGTGC GATCGAGCGT TTCCCGAACG ATTTCTGTCG TCAACGGGGG CAGGGGACGT	1260
TCTGGCCGTG CGACGAGAAC CGAGCCTTCC CGAACGAGTT CGACACCGGT CGGGGCCGGC	1320
TCAATCTCGA TGCGCCCATC GCGCTCGGTG ATCTCCACCT GGTCGTTCCC GCGCAAGCCA	1380
AGGCGCTCGC GAATCCGCTT GGGAATCACC AGACGTCTTG CGACATCGAT GGTGTTCGC	1440
ATGGTAGGAA ATTTACCATC GCACGTTCCA TAGGCGTGTC CTGCGCGGGA TGTCGGGACG	1500
ATCCGCTAGC GTATCGAACG ATTGTTTCGG AAATGGCTGA GGGAGCGTGC GGTGCGGGTG	1560
ATGGGTGTG ATCCCGGGT GACCCGATGC GGGCTGTGCG TCATCGAGAG TGGGCGTGGT	1620
CGGCAGCTCA CCGCGCTGGA TGTCGACGTG GTGCGCACAC CGTCGGATGC GGCCTTGCG	1680
CAGCGCCTGT TGGCCATCAG CGATGCCGTC GAGCACTGGC TGGACACCCA TCATCCGGAG	1740
GTGGTGGCTA TCGAACGGGT GTTCTCTCAG CTCAACGTGA CCACGGTGAT GGGCACCGCG	1800
CAGGCCGGCG GCGTGATCGC CCTGGCGGCG GCCAAACGTG GTGTCGACGT GCATTTCCAT	1860
ACCCCCAGCG AGGTCAAGGC GCGGCTCACT GGCAACGGTT CCGCAGACAA GGCTCAGGTC	1920
ACC	1923

(2) INFORMATION FOR SEQ ID NO:191:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1055 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:191:

CTGGCGTGCC AGTGTACCG GCGATATGAC GTCGGCATTC AATTTCGCGG CCCC GCCGGA	60
CCCGTCGCCA CCCAATCTGG ACCACCCGGT CCGTCAATTG CCGAAGGTCG CCAAGTGCGT	120
GCCCAATGTG GTGCTGGGTT TCTTGAACGA AGGCCTGCCG TATCGGGTGC CCTACCCCCA	180
AACAACGCCA GTCCAGGAAT CCGGTCCCGC GCGGCCGATT CCCAGCGGCA TCTGCTAGCC	240
GGGGATGGTT CAGACGTAAC GGTTGGCTAG GTCGAAACCC GCGCCAGGGC CGCTGGACGG	300
GCTCATGGCA GCGAAATTAG AAAACCCGGG ATATTGTCCG CGGATTGTCA TACGATGCTG	360

AGTGCTTGGT GGTTCGTGTT TAGCCATTGA GTGTGGATGT GTTGAGACCC TGGCCTGGAA	420
GGGGACAACG TGCTTTTGCC TCTTGGTCCG CCTTTGCCGC CCGACGCGGT GGTGGCGAAA	480
CGGGCTGAGT CGGGAATGCT CGGCGGGTTG TCGGTTCCGC TCAGCTGGGG AGTGGCTGTG	540
CCACCCGATG ATTATGACCA CTGGGCGCCT GCGCCGAGG ACGGCGCCGA TGTCGATGTC	600
CAGGCGGCCG AAGGGGCGGA CGCAGAGGCC GCGGCCATGG ACGAGTGGGA TGAGTGGCAG	660
GCGTGGAACG AGTGGGTGGC GGAGAACGCT GAACCCCGCT TTGAGGTGCC ACGGAGTAGC	720
AGCAGCGTGA TTCCGCATTC TCCGGCGGCC GGCTAGGAGA GGGGGCGCAG ACTGTCGTTA	780
TTTGACCAGT GATCGGCGGT CTCGGTGTTT CCGCGGCCGG CTATGACAAC AGTCAATGTG	840
CATGACAAGT TACAGGTATT AGGTCCAGGT TCAACAAGGA GACAGGCAAC ATGGCAACAC	900
GTTTTATGAC GGATCCGCAC GCGATGCGGG ACATGGCGGG CCGTTTTGAG GTGCACGCCC	960
AGACGGTGGA GGACGAGGCT CGCCGGATGT GGGCGTCCGC GCAAAACATC TCGGGNGCGG	1020
GCTGGAGTGG CATGGCCGAG GCGACCTCGC TAGAC	1055

(2) INFORMATION FOR SEQ ID NO:192:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 359 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:192:

CCGCCTCGTT GTTGGCATAC TCCGCCGCGG CCGCCTCGAC CGCACTGGCC GTGGCGTGTG	60
TCCGGGCTGA CCACCGGGAT CGCCGAACCA TCCGAGATCA CCTCGCAATG ATCCACCTCG	120
CGCAGCTGGT CACCCAGCCA CCGGGCGGTG TGCGACAGCG CCTGCATCAC CTTGGTATAG	180
CCGTCGCGCC CCAGCCGCGA GAAGTTGTAG TACTGGCCCA CCACCTGGTT ACCGGGACGG	240
GAGAAGTTCA GGTGAAGGT CGGCATGTCG CCGCCGAGGT AGTTGACCCG GAAAACCGA	300
TCCTCCGGCA GGTGCTCGGG CCCGCGCCAC ACGACAAACC CGACGCCGGG ATAGGTCAG	359

(2) INFORMATION FOR SEQ ID NO:193:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 350 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:193:

AACGGGCCCCG TGGGCACCGC TCCTCTAAGG GCTCTCGTTG GTCGCATGAA GTGCTGGAAG	60
GATGCATCTT GGCAGATTCC CGCCAGAGCA AAACAGCCGC TAGTCCTAGT CCGAGTCGCC	120
CGCAAAGTTC CTCGAATAAC TCCGTACCCG GAGCGCCAAA CCGGGTCTCC TTCGCTAAGC	180
TGCGCGAACC ACTTGAGGTT CCGGGACTCC TTGACGTCCA GACCGATTCTG TTCGAGTGGC	240
TGATCGGTTT GCCGCGCTGG CGCGAATCCG CCGCCGAGCG GGGTGATGTC AACCCAGTGG	300
GTGGCCTGGA AGAGGTGCTC TACGAGCTGT CTCCGATCGA GGA CTTCTCC	350

(2) INFORMATION FOR SEQ ID NO:194:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 679 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:194:

Glu	Gln	Pro	Lys	Gly	Pro	Phe	Gly	Glu	Val	Ile	Glu	Ala	Phe	Ala	Asp	1	5	10	15
Gly	Leu	Ala	Gly	Lys	Gly	Lys	Gln	Ile	Asn	Thr	Thr	Leu	Asn	Ser	Leu	20	25	30	
Ser	Gln	Ala	Leu	Asn	Ala	Leu	Asn	Glu	Gly	Arg	Gly	Asp	Phe	Phe	Ala	35	40	45	
Val	Val	Arg	Ser	Leu	Ala	Leu	Phe	Val	Asn	Ala	Leu	His	Gln	Asp	Asp	50	55	60	
Gln	Gln	Phe	Val	Ala	Leu	Asn	Lys	Asn	Leu	Ala	Glu	Phe	Thr	Asp	Arg	65	70	75	80
Leu	Thr	His	Ser	Asp	Ala	Asp	Leu	Ser	Asn	Ala	Ile	Gln	Gln	Phe	Asp	85	90	95	
Ser	Leu	Leu	Ala	Val	Ala	Arg	Pro	Phe	Phe	Ala	Lys	Asn	Arg	Glu	Val	100	105	110	
Leu	Thr	His	Asp	Val	Asn	Asn	Leu	Ala	Thr	Val	Thr	Thr	Thr	Leu	Leu	115	120	125	
Gln	Pro	Asp	Pro	Leu	Asp	Gly	Leu	Glu	Thr	Val	Leu	His	Ile	Phe	Pro	130	135	140	
Thr	Leu	Ala	Ala	Asn	Ile	Asn	Gln	Leu	Tyr	His	Pro	Thr	His	Gly	Gly	145	150	155	160
Val	Val	Ser	Leu	Ser	Ala	Phe	Thr	Asn	Phe	Ala	Asn	Pro	Met	Glu	Phe	165	170	175	

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Ile	Cys	Ser	Ser	Ile	Gln	Ala	Gly	Ser	Arg	Leu	Gly	Tyr	Gln	Glu	Ser	
			180					185					190			
Ala	Glu	Leu	Cys	Ala	Gln	Tyr	Leu	Ala	Pro	Val	Leu	Asp	Ala	Ile	Lys	
		195					200					205				
Phe	Asn	Tyr	Phe	Pro	Phe	Gly	Leu	Asn	Val	Ala	Ser	Thr	Ala	Ser	Thr	
	210					215					220					
Leu	Pro	Lys	Glu	Ile	Ala	Tyr	Ser	Glu	Pro	Arg	Leu	Gln	Pro	Pro	Asn	
225					230					235					240	
Gly	Tyr	Lys	Asp	Thr	Thr	Val	Pro	Gly	Ile	Trp	Val	Pro	Asp	Thr	Pro	
				245					250					255		
Leu	Ser	His	Arg	Asn	Thr	Gln	Pro	Gly	Trp	Val	Val	Ala	Pro	Gly	Met	
			260					265					270			
Gln	Gly	Val	Gln	Val	Gly	Pro	Ile	Thr	Gln	Gly	Leu	Leu	Thr	Pro	Glu	
		275					280					285				
Ser	Leu	Ala	Glu	Leu	Met	Gly	Gly	Pro	Asp	Ile	Ala	Pro	Pro	Ser	Ser	
	290					295					300					
Gly	Leu	Gln	Thr	Pro	Pro	Gly	Pro	Pro	Asn	Ala	Tyr	Asp	Glu	Tyr	Pro	
305					310					315					320	
Val	Leu	Pro	Pro	Ile	Gly	Leu	Gln	Ala	Pro	Gln	Val	Pro	Ile	Pro	Pro	
				325					330					335		
Pro	Pro	Pro	Gly	Pro	Asp	Val	Ile	Pro	Gly	Pro	Val	Pro	Pro	Val	Leu	
			340					345					350			
Ala	Ala	Ile	Val	Phe	Pro	Arg	Asp	Arg	Pro	Ala	Ala	Ser	Glu	Asn	Phe	
		355					360					365				
Asp	Tyr	Met	Gly	Leu	Leu	Leu	Leu	Ser	Pro	Gly	Leu	Ala	Thr	Phe	Leu	
	370					375					380					
Phe	Gly	Val	Ser	Ser	Ser	Pro	Ala	Arg	Gly	Thr	Met	Ala	Asp	Arg	His	
385					390					395					400	
Val	Leu	Ile	Pro	Ala	Ile	Thr	Gly	Leu	Ala	Leu	Ile	Ala	Ala	Phe	Val	
				405					410					415		
Ala	His	Ser	Trp	Tyr	Arg	Thr	Glu	His	Pro	Leu	Ile	Asp	Met	Arg	Leu	
			420					425					430			
Phe	Gln	Asn	Arg	Ala	Val	Ala	Gln	Ala	Asn	Met	Thr	Met	Thr	Val	Leu	
		435					440					445				
Ser	Leu	Gly	Leu	Phe	Gly	Ser	Phe	Leu	Leu	Leu	Pro	Ser	Tyr	Leu	Gln	
	450					455					460					
Gln	Val	Leu	His	Gln	Ser	Pro	Met	Gln	Ser	Gly	Val	His	Ile	Ile	Pro	
465					470					475					480	
Gln	Gly	Leu	Gly	Ala	Met	Leu	Ala	Met	Pro	Ile	Ala	Gly	Ala	Met	Met	
				485					490					495		
Asp	Arg	Arg	Gly	Pro	Ala	Lys	Ile	Val	Leu	Val	Gly	Ile	Met	Leu	Ile	
			500					505					510			

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Ala Ala Gly Leu Gly Thr Phe Ala Phe Gly Val Ala Arg Gln Ala Asp
515 520 525

Tyr Leu Pro Ile Leu Pro Thr Gly Leu Ala Ile Met Gly Met Gly Met
530 535 540

Gly Cys Ser Met Met Pro Leu Ser Gly Ala Ala Val Gln Thr Leu Ala
545 550 555 560

Pro His Gln Ile Ala Arg Gly Ser Thr Leu Ile Ser Val Asn Gln Gln
565 570 575

Val Gly Gly Ser Ile Gly Thr Ala Leu Met Ser Val Leu Leu Thr Tyr
580 585 590

Gln Phe Asn His Ser Glu Ile Ile Ala Thr Ala Lys Lys Val Ala Leu
595 600 605

Thr Pro Glu Ser Gly Ala Gly Arg Gly Ala Ala Val Asp Pro Ser Ser
610 615 620

Leu Pro Arg Gln Thr Asn Phe Ala Ala Gln Leu Leu His Asp Leu Ser
625 630 635 640

His Ala Tyr Ala Val Val Phe Val Ile Ala Thr Ala Leu Val Val Ser
645 650 655

Thr Leu Ile Pro Ala Ala Phe Leu Pro Lys Gln Gln Ala Ser His Arg
660 665 670

Arg Ala Pro Leu Leu Ser Ala
675

(2) INFORMATION FOR SEQ ID NO:195:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 120 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:195:

Thr Pro Glu Lys Ser Phe Val Asp Asp Leu Asp Ile Asp Ser Leu Ser
1 5 10 15

Met Val Glu Ile Ala Val Gln Thr Glu Asp Lys Tyr Gly Val Lys Ile
20 25 30

Pro Asp Glu Asp Leu Ala Gly Leu Arg Thr Val Gly Asp Val Val Ala
35 40 45

Tyr Ile Gln Lys Leu Glu Glu Glu Asn Pro Glu Ala Ala Gln Ala Leu
50 55 60

Arg Ala Lys Ile Glu Ser Glu Asn Pro Asp Ala Ala Arg Ala Asp Arg
65 70 75 80

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Cys Val Ser Pro Thr Ser Gln Ala Arg Asp Ala Arg Arg Pro Leu Ala
 85 90 95

Arg Ser Ala Arg Leu Ala Cys Arg Arg Leu Pro Ala Ser Val Pro Thr
 100 105 110

Thr Arg Arg Asp Pro Arg Glu Arg
 115 120

(2) INFORMATION FOR SEQ ID NO:196:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 89 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:196:

Leu Ala Cys Gln Cys His Arg Arg Tyr Asp Val Gly Ile Gln Phe Arg
 1 5 10 15

Gly Pro Ala Gly Pro Val Ala Thr Gln Ser Gly Pro Pro Gly Pro Ser
 20 25 30

Ile Ala Glu Gly Arg Gln Val Arg Ala Gln Cys Gly Ala Gly Phe Leu
 35 40 45

Glu Arg Arg Pro Ala Val Ser Gly Ala Leu Pro Pro Asn Asn Ala Ser
 50 55 60

Pro Gly Ile Arg Ser Arg Ala Ala Asp Ser Gln Arg His Leu Leu Ala
 65 70 75 80

Gly Asp Gly Ser Asp Val Thr Val Gly
 85

(2) INFORMATION FOR SEQ ID NO:197:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 119 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:197:

Ala Ser Leu Leu Ala Tyr Ser Ala Ala Ala Ala Ser Thr Ala Leu Ala
 1 5 10 15

Val Ala Cys Val Arg Ala Asp His Arg Asp Arg Arg Thr Ile Arg Asp
 20 25 30

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His Leu Ala Met Ile His Leu Ala Gln Leu Val Thr Gln Pro Pro Gly
 35                      40                      45

Gly Val Arg Gln Arg Leu His His Leu Gly Ile Ala Val Ala Pro Gln
 50                      55                      60

Pro Gln Glu Val Val Val Leu Ala His His Leu Val Thr Gly Thr Gly
65                      70                      75                      80

Glu Val Gln Gly Glu Gly Arg His Val Ala Ala Glu Val Val Asp Pro
                        85                      90                      95

Glu Asn Gln Ile Leu Arg Gln Val Leu Gly Pro Ala Pro His Asp Lys
          100                      105                      110

Pro Asp Ala Gly Ile Gly Gln
          115

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(2) INFORMATION FOR SEQ ID NO:198:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 116 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:198:

```

Arg Ala Arg Gly His Arg Ser Ser Lys Gly Ser Arg Trp Ser His Glu
1                      5                      10                      15

Val Leu Glu Gly Cys Ile Leu Ala Asp Ser Arg Gln Ser Lys Thr Ala
          20                      25                      30

Ala Ser Pro Ser Pro Ser Arg Pro Gln Ser Ser Ser Asn Asn Ser Val
          35                      40                      45

Pro Gly Ala Pro Asn Arg Val Ser Phe Ala Lys Leu Arg Glu Pro Leu
50                      55                      60

Glu Val Pro Gly Leu Leu Asp Val Gln Thr Asp Ser Phe Glu Trp Leu
65                      70                      75                      80

Ile Gly Ser Pro Arg Trp Arg Glu Ser Ala Ala Glu Arg Gly Asp Val
          85                      90                      95

Asn Pro Val Gly Gly Leu Glu Glu Val Leu Tyr Glu Leu Ser Pro Ile
          100                      105                      110

Glu Asp Phe Ser
          115

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(2) INFORMATION FOR SEQ ID NO:199:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 811 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:199:

TGCTACGCAG CAATCGCTTT GGTGACAGAT GTGGATGCCG GCGTCGCTGC TGGCGATGGC	60
GTGAAAGCCG CCGACGTGTT CGCCGCATTC GGGGAGAACA TCGAACTGCT CAAAAGGCTG	120
GTGCGGGCCG CCATCGATCG GGTGCGCCGAC GAGCGCACGT GCACGCACTG TCAACACCAC	180
GCCGGTGTTT CGTTGCCGTT CGAGCTGCCA TGAGGGTGCT GCTGACCGGC GCGGCCGGCT	240
TCATCGGGTC GCGCGTGGAT GCGGCGTTAC GGGCTGCGGG TCACGACGTG GTGGGCGTCG	300
ACGCGCTGCT GCCCGCCGCG CACGGGCCAA ACCCGGTGCT GCCACCGGGC TGCCAGCGGG	360
TCGACGTGCG CGACGCCAGC GCGCTGGCCC CGTTGTTGGC CGGTGTCGAT CTGGTGTGTC	420
ACCAGGCCGC CATGGTGGGT GCCGGCGTCA ACGCCGCCGA CGCACCCGCC TATGGCGGCC	480
ACAACGATTT CGCCACCACG GTGCTGCTGG CGCAGATGTT CGCCGCCGGG GTCCGCCGTT	540
TGGTGCTGGC GTCGTGATG GTGGTTTACG GGCAGGGGCG CTATGACTGT CCCCAGCATG	600
GACCGGTCGA CCCGCTGCCG CGGCGGCGAG CCGACCTGGA CAATGGGGTC TTCGAGCACC	660
GTTGCCCGGG GTGCGGCGAG CCAGTCATCT GGCAATTGGT CGACGAAGAT GCCCCGTGTC	720
GCCCCGCGCAG CCTGTACGCG GCAGCAAGAC CGCGCAGGAG CACTACGCGC TGGCGTGGTC	780
GGAAACGAAT GCGGTTCCG TGGTGGCGTT G	811

(2) INFORMATION FOR SEQ ID NO:200:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 966 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:200:

GTCCCGCGAT GTGGCCGAGC ATGACTTTTCG GCAACACCGG CGTAGTAGTC GAAGATATCG	60
GACTTTGTGG TCCCGGTGGC GGGATAGAGC ACCTGTCGGC GTTGGTCAGC GTCACCCGTT	120
GCTCGGACGC CGAACCCATG CTTTCAACGT AGCCTGTCGG TCACACAAGT CGCGAGCGTA	180
ACGTCACGGT CAAATATCGC GTGGAATTTT CCGTGACGT TCCGCTCGCG GACAATCAAG	240
GCATACTCAC TTACATGCGA GCCATTTGGA CGGGTTCGAT CGCCTTCGGG CTGGTGAACG	300
TGCCGGTCAA GGTGTACAGC GCTACCGCAG ACCACGACAT CAGGTTCCAC CAGGTGCACG	360

CCAAGGACAA CGGACGCATC CGGTACAAGC GCGTCTGCGA GGCGTGTGGC GAGGTGGTCG	420
ACTACCGCGA TCTTGCCCGG GCCTACGAGT CCGGCGACGG CCAAATGGTG GCGATCACCG	480
ACGACGACAT CGCCAGCTTG CCTGAAGAAC GCAGCCGGGA GATCGAGGTG TTGGAGTTCTG	540
TCCCCGCCGC CGACGTGGAC CCGATGATGT TCGACCGCAG CTACTTTTTG GAGCCTGATT	600
CGAAGTCGTC GAAATCGTAT GTGCTGCTGG CTAAGACACT CGCCGAGACC GACCGGATGG	660
CGATCGTGGA TCGCCCCACC GGCCGTGAAT GCAGGAAAAA TAAGAGCCGC TATCCACAAT	720
TCGGCGTCGA GCTCGGCTAC CACAAACGGT AGAACGATCG AGACATTCCC GAGCTGAAAT	780
GCGGCGCTAT AGAAGCCGCT CTGCGCGATT ATCAAACGCA AAATACGCTT ACTCATGCCA	840
TCGGCGCTGC TCACCCGATG CGACGTTTTT GCCACGCTCC ACCGCCTGCC GCGCGACCTC	900
AAGTGGGCAT GCATCCCACC CGTTCCCGGA AACCGGTTCC GGCGGGTCGG CTCATCGCTT	960
CATCCT	966

(2) INFORMATION FOR SEQ ID NO:201:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2367 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:201:

CCGCACCGCC GGCAATACCG CCAGCGCCAC CGTTACCGCC GTTTGCGCCG TTGCCCCCGT	60
TGCCGCCCCGT CCCGCCGGCC CCGCCGATGG AGTTCTCATC GCCAAAAGTA CTGGCGTTGC	120
CACCGGAGCC GCCGTTGCCG CCGTCACCGC CAGCCCCGCC GACTCCACCG GCCCCACCGA	180
CTCCGCCGCT GCCACCGTTG CCGCCGTTGC CGATCAACAT GCCGCTGGCG CCACCCTTGC	240
CACCCACGCC ACCGGCTCCG CCCACCCCGC CGACACCAAG CGAGCTGCCG CCGGAGCCAC	300
CATCACCACC TACGCCACCG ACCGCCAGA CACCAGCGAC CGGGTCTTCG TGAAACGTCG	360
CGGTGCCACC ACCGCCGCCG TTACCGCCAA CCCACCGGC AACGCCGGCG CCGCCATCCC	420
CGCCGGCCCC GCGTTGCCG CCGTTGCCGC CGTTGCCGAA CAACAACCCG CCGGCGCCGC	480
CGTTGCCGCC CGCGCCGCCG GTCCCGCCGG CGCCGCCGAC GCAAGGCCG CTGCCGCCCT	540
TGCCGCCATC ACCACCCTTG CCGCCGACCA CATCGGGTTC TGCTCGGGG TCTGGGCTGT	600
CAACCTCGC GATGCCAGCG TTGCCGCCGC TTCCCCGGG CCCCCCGTG GCGCCGTCAC	660
CACCGATACC ACCCGCGCCA CCGGCGCCAC CGTTGCCGCC ATCACCGAAT AGCAACCCGC	720
CGGCGCCACC ATTGCCGCCA GTCGCCCTG CGCCACCGTC GGCGCCGGAG GCGGCACTGG	780

CAGCCCCGTT	ACCACCGAAA	CCGCCGCTAC	CACCGGTAGA	GGTGGCAGTG	GCGATGTGTA	840
CGAAAGCGCC	GCCTCCGGCG	CCGCCGCTAC	CACCCCCACT	GCCGGCGGGCT	ACACCGTCGG	900
ACCCGTTGCC	ACCATCACCG	CCAAAGGCGC	TCGCAATGTC	GCCCTGCGCG	ACTCCGCCGT	960
CGCCGCCGTT	GCCGCCGCGG	CCACCGGCAG	CGGCGGTACC	GCCGTCACCA	CCGGCACCGC	1020
CGGTGGCCTT	GCCCCAGCCT	GCCGTCGCGG	TGGCACCGTC	GCCGCCGGTG	CCACCGGTCTG	1080
GCGTGCCGGC	AGTGCCATGG	CCGCCCGTGC	CGCCGTCGCC	GCCGGTTTGA	TCACCGATGC	1140
CGGACACATC	TGCCGGGCTG	TCCCCGGTGC	TGGCCGCGGG	GCCGGGCGTG	GGATTGACCC	1200
CGTTTGCCCC	GGCGAGGCCG	GCGCCGCCGG	TACCACCGGC	GCCGCCATGG	CCGAACAGCC	1260
CGGCGTTGCC	GCCGTTACCG	CCCGCACCCC	CGATGCCTGC	GGCCACGCTG	GTGCCGCCGA	1320
CACCGCCGTT	GCCGCCGTTG	CCCCACAACC	ACCCCCCGTT	CCCACCGGCA	CCGCCGGCCG	1380
CGCCGGTACC	ACCGGCCCCG	CCGTTGCCGC	CGTTGCCGAT	CAACCCGGCC	GCGCCTCCGC	1440
TGCCGCCGGT	TTGACCGAAC	CCGCCAGCCG	CGCCGTTGCC	ACCGTTGCCA	AACAGCAACC	1500
CGCCGGCCGC	GCCAGGCTGC	CCGGGTGCCG	TCCCGTCGGC	GCCGTTTCCG	ATCAACGGGC	1560
GCCCCAAAAG	CGCCTCGGTG	GGCGCATTCA	CCGCACCCAG	CAGACTCCGC	TCAACAGCGG	1620
CTTCAGTGCT	GGCATAACGA	CCCGCGGCCG	CAGTCAACGC	CTGCACAAAC	TGCTCGTGAA	1680
ACGCTGCCAC	CTGTACGCTG	AGCGCCTGAT	ACTGCCGAGC	ATGGGCCCCG	AACAACCCCCG	1740
CAATCGCCGC	CGACACTTCA	TCGGCAGCCG	CAGCCACCAC	TTCCGTCGTC	GGGATCGCCG	1800
CGGCCGCATT	AGCCGCGCTC	ACCTGCGAAC	CAATAGTCGA	TAAATCCAAA	GCCGCAGTTG	1860
CCAGCAGCTG	CGGCGTCGCG	ATCACCAAGG	ACACCTCGCA	CCTCCGATA	CCCCATATCG	1920
CCGCACCGTG	TCCCCAGCGG	CCACGTGACC	TTTGGTCGCT	GGCTGGCGGC	CCTGACTATG	1980
GCCGCGACGG	CCCTCGTTCT	GATTTCGCCCC	GGCGCGCAGC	TTGTTGCGCG	AGTTGAAGAC	2040
GGGAGGACAG	GCCGAGCTTG	GTGTAGACGT	GGGTCAAGTG	GGAATGCACG	GTCCGCGGCG	2100
AGATGAATAG	GCGGACGCCG	ATCTCCTTGT	TGCTGAGTCC	CTCACCGACC	AGTAGAGCCA	2160
CCTCAAGCTC	TGTCGGTGTC	AACGCGCCCC	AGCCACTTGT	CGGGCGTTTC	CGTGCACCGC	2220
GGCCTCGTTG	CGCGTACGCG	ATCGCCTCAT	CGATCGATAA	CGCAGTTCCT	TCGGCCCAGG	2280
CATCGTCGAA	CTCGCTGTCA	CCCATGGATT	TTCGAAGGGT	GGCTAGCGAC	GAGTTACAGC	2340
CCGCCTGGTA	GATCCCGAAG	CGGACCG				2367

(2) INFORMATION FOR SEQ ID NO:202:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 376 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:202:

Gln	Pro	Ala	Gly	Ala	Thr	Ile	Ala	Ala	Ser	Ser	Pro	Cys	Ala	Thr	Val	1	5	10	15
Gly	Ala	Gly	Gly	Gly	Thr	Gly	Ser	Pro	Val	Thr	Thr	Glu	Thr	Ala	Ala	20	25	30	
Thr	Thr	Gly	Arg	Gly	Gly	Ser	Gly	Asp	Val	Tyr	Glu	Ser	Ala	Ala	Ser	35	40	45	
Gly	Ala	Ala	Ala	Thr	Thr	Pro	Thr	Ala	Gly	Gly	Tyr	Thr	Val	Gly	Pro	50	55	60	
Val	Ala	Thr	Ile	Thr	Ala	Lys	Gly	Ala	Arg	Asn	Val	Ala	Leu	Arg	Asp	65	70	75	80
Ser	Ala	Val	Ala	Ala	Val	Ala	Ala	Ala	Ala	Thr	Gly	Ser	Gly	Gly	Thr	85	90	95	
Ala	Val	Thr	Thr	Gly	Thr	Ala	Gly	Gly	Leu	Ala	Arg	Ala	Cys	Arg	Arg	100	105	110	
Gly	Gly	Thr	Val	Ala	Ala	Gly	Ala	Thr	Gly	Arg	Arg	Ala	Gly	Ser	Ala	115	120	125	
Met	Ala	Ala	Arg	Ala	Ala	Val	Ala	Ala	Gly	Leu	Ile	Thr	Asp	Ala	Gly	130	135	140	
His	Ile	Cys	Arg	Ala	Val	Pro	Gly	Ala	Gly	Arg	Gly	Ala	Gly	Arg	Gly	145	150	155	160
Ile	Asp	Pro	Val	Cys	Pro	Gly	Glu	Ala	Gly	Ala	Ala	Gly	Thr	Thr	Gly	165	170	175	
Ala	Ala	Met	Ala	Glu	Gln	Pro	Gly	Val	Ala	Ala	Val	Thr	Ala	Arg	Thr	180	185	190	
Pro	Asp	Ala	Cys	Gly	His	Ala	Gly	Ala	Ala	Asp	Thr	Ala	Val	Ala	Ala	195	200	205	
Val	Ala	Pro	Gln	Pro	Pro	Pro	Val	Pro	Thr	Gly	Thr	Ala	Gly	Arg	Ala	210	215	220	
Gly	Thr	Thr	Gly	Pro	Ala	Val	Ala	Ala	Val	Ala	Asp	Gln	Pro	Gly	Arg	225	230	235	240
Ala	Ser	Ala	Ala	Ala	Gly	Leu	Thr	Glu	Pro	Ala	Ser	Arg	Ala	Val	Ala	245	250	255	
Thr	Val	Ala	Lys	Gln	Gln	Pro	Ala	Gly	Arg	Ala	Arg	Leu	Pro	Gly	Cys	260	265	270	
Arg	Pro	Val	Gly	Ala	Val	Ser	Asp	Gln	Arg	Ala	Pro	Gln	Lys	Arg	Leu	275	280	285	
Gly	Gly	Arg	Ile	His	Arg	Thr	Gln	Gln	Thr	Pro	Leu	Asn	Ser	Gly	Phe	290	295	300	

197

Ser Ala Gly Ile Pro Thr Arg Gly Arg Ser Gln Arg Leu His Lys Leu
 305 310 315 320

Leu Val Lys Arg Cys His Leu Tyr Ala Glu Arg Leu Ile Leu Pro Ser
 325 330 335

Met Gly Pro Glu Gln Pro Arg Asn Arg Arg Arg His Phe Ile Gly Ser
 340 345 350

Arg Ser His His Phe Arg Arg Arg Asp Arg Arg Gly Arg Ile Ser Arg
 355 360 365

Ala His Leu Arg Thr Asn Ser Arg
 370 375

(2) INFORMATION FOR SEQ ID NO:203:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2852 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:203:

GGCCAAAACG CCCCGGCGAT CGCGGCCACC GAGGCCGCCT ACGACCAGAT GTGGGCCCAG	60
GACGTGGCGG CGATGTTTGG CTACCATGCC GGGGCTTCGG CGGCCGTCTC GGCGTTGACA	120
CCGTTCGGCC AGGCGCTGCC GACCGTGGCG GGCGGCGGTG CGCTGGTCAG CGCGGCCCGC	180
GCTCAGGTGA CCACGCGGGT CTTCCGCAAC CTGGGCTTGG CGAACGTCCG CGAGGGCAAC	240
GTCCGCAACG GTAATGTCCG GAACTTCAAT CTCGGCTCGG CCAACATCGG CAACGGCAAC	300
ATCGGCAGCG GCAACATCGG CAGCTCCAAC ATCGGGTTTG GCAACGTGGG TCCTGGGTTG	360
ACCGCAGCGC TGAACAACAT CGGTTTCGGC AACACCGGCA GCAACAACAT CGGGTTTGGC	420
AACACCGGCA GCAACAACAT CGGGTTCGGC AATACCGGAG ACGGCAACCG AGGTATCGGG	480
CTCACGGGTA GCGGTTTGTT GGGGTTTCGGC GGCTGAACT CGGGCACCGG CAACATCGGT	540
CTGTTCAACT CGGGCACCGG AAACGTTCGGC ATCGGCAACT CGGGTACCGG GAACTGGGGC	600
ATTGGCAACT CGGGCAACAG CTACAACACC GGTTTTGGCA ACTCCGGCGA CGCCAACACG	660
GGCTTCTTCA ACTCCGGAAT AGCCAACACC GGCGTCGGCA ACGCCGGCAA CTACAACACC	720
GGTAGCTACA ACCCGGGCAA CAGCAATACC GGCGGCTTCA ACATGGGCCA GTACAACACG	780
GGCTACCTGA ACAGCGGCAA CTACAACACC GGCTTGCAA ACTCCGGCAA TGTCAACACC	840
GGCGCCTTCA TTA CTGGCAA CTTCAACAAC GGCTTCTTGT GGCGCGGCGA CCACCAAGGC	900
CTGATTTTCG GGAGCCCCGG CTTCTTCAAC TCGACCAGTG CGCCGTCGTC GGGATTCTTC	960

AACAGCGGTG	CCGGTAGCGC	GTCCGGCTTC	CTGAACTCCG	GTGCCAACAA	TTCTGGCTTC	1020
TTCAACTCTT	CGTCGGGGGC	CATCGGTAAAC	TCCGGCCTGG	CAAACGCGGG	CGTGCTGGTA	1080
TCGGGCGTGA	TCAACTCGGG	CAACACCGTA	TCGGGTTTGT	TCAACATGAG	CCTGGTGGCC	1140
ATCACAAACGC	CGGCCTTGAT	CTCGGGCTTC	TTCAACACCG	GAAGCAACAT	GTCGGGATTT	1200
TTCGGTGGCC	CACCGGTCTT	CAATCTCGGC	CTGGCAAACC	GGGGCGTCGT	GAACATTCTC	1260
GGCAACGCCA	ACATCGGCAA	TTACAACATT	CTCGGCAGCG	GAAACGTCGG	TGACTTCAAC	1320
ATCCTTGGCA	GCGGCAACCT	CGGCAGCCAA	AACATCTTGG	GCAGCGGCAA	CGTCGGCAGC	1380
TTCAATATCG	GCAGTGGAAA	CATCGGAGTA	TTCAATGTCG	GTTCCGGAAG	CCTGGGAAAC	1440
TACAACATCG	GATCCGGAAA	CCTCGGGATC	TACAACATCG	GTTTTGGAAA	CGTCGGCGAC	1500
TACAACGTCG	GCTTCGGGAA	CGCGGGCGAC	TTCAACCAAG	GCTTTGCCAA	CACCGGCAAC	1560
AACAACATCG	GGTTCGCCAA	CACCGGCAAC	AACAACATCG	GCATCGGGCT	GTCCGGCGAC	1620
AACCAGCAGG	GCTTCAATAT	TGCTAGCGGC	TGGAACTCGG	GCACCGGCAA	CAGCGGCCTG	1680
TTCAATTCTGG	GCACCAATAA	CGTTGGCATC	TTCAACGCGG	GCACCGGAAA	CGTCGGCATC	1740
GCAAACCTCGG	GCACCGGGAA	CTGGGGTATC	GGGAACCCGG	GTACCGACAA	TACCGGCATC	1800
CTCAATGCTG	GCAGCTACAA	CACGGGCATC	CTCAACGCCG	GCGACTTCAA	CACGGGCTTC	1860
TACAACACGG	GCAGCTACAA	CACCGGCGGC	TTCAACGTCG	GTAACACCAA	CACCGGCAAC	1920
TTCAACGTGG	GTGACACCAA	TACCGGCAGC	TATAACCCGG	GTGACACCAA	CACCGGCTTC	1980
TTCAATCCCG	GCAACGTCAA	TACCGGCGCT	TTGACACGG	GCGACTTCAA	CAATGGCTTC	2040
TTGGTGGCGG	GCGATAACCA	GGGCCAGATT	GCCATCGATC	TCTCGGTCAC	CACTCCATTC	2100
ATCCCCATAA	ACGAGCAGAT	GGTCATTGAC	GTACACAACG	TAATGACCTT	CGGCGGCAAC	2160
ATGATCACGG	TCACCGAGGC	CTCGACCGTT	TTCCCCAAA	CCTTCTATCT	GAGCGGTTTG	2220
TTCTTCTTCG	GCCCGGTCAA	TCTCAGCGCA	TCCACGCTGA	CCGTTCCGAC	GATCACCTC	2280
ACCATCGGCG	GACCGACGGT	GACCGTCCCC	ATCAGCATTG	TCGGTGCTCT	GGAGAGCCGC	2340
ACGATTACCT	TCCTCAAGAT	CGATCCGGCG	CCGGGCATCG	GAAATTCGAC	CACCAACCCC	2400
TCGTCCGGCT	TCTTCAACTC	GGGCACCGGT	GGCACATCTG	GCTTCCAAAA	CGTCGGCGGC	2460
GGCAGTTCAG	GCGTCTGGAA	CAGTGGTTTG	AGCAGCGCGA	TAGGGAATTC	GGGTTTCCAG	2520
AACCTCGGCT	CGCTGCAGTC	AGGCTGGGCG	AACCTGGGCA	ACTCCGTATC	GGGCTTTTTTC	2580
AACACCAGTA	CGGTGAACCT	CTCCACGCCG	GCCAATGTCT	CGGGCCTGAA	CAACATCGGC	2640
ACCAACCTGT	CCGGCGTGTT	CCGCGGTCCG	ACCGGGACGA	TTTTCAACGC	GGGCCTTGCC	2700
AACCTGGGCC	AGTTGAACAT	CGGCAGCGCC	TCGTGCCGAA	TTCCGGCACGA	GTTAGATACG	2760
GTTTCAACAA	TCATATCCGC	GTTTTGCGGC	AGTGCATCAG	ACGAATCGAA	CCCGGGAAGC	2820

GTAAGCGAAT AAACCGAATG GCGGCCTGTC AT

2852

(2) INFORMATION FOR SEQ ID NO:204:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 943 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:204:

Gly Gln Asn Ala Pro Ala Ile Ala Ala Thr Glu Ala Ala Tyr Asp Gln
 1 5 10 15
 Met Trp Ala Gln Asp Val Ala Ala Met Phe Gly Tyr His Ala Gly Ala
 20 25 30
 Ser Ala Ala Val Ser Ala Leu Thr Pro Phe Gly Gln Ala Leu Pro Thr
 35 40 45
 Val Ala Gly Gly Gly Ala Leu Val Ser Ala Ala Ala Ala Gln Val Thr
 50 55 60
 Thr Arg Val Phe Arg Asn Leu Gly Leu Ala Asn Val Arg Glu Gly Asn
 65 70 75 80
 Val Arg Asn Gly Asn Val Arg Asn Phe Asn Leu Gly Ser Ala Asn Ile
 85 90 95
 Gly Asn Gly Asn Ile Gly Ser Gly Asn Ile Gly Ser Ser Asn Ile Gly
 100 105 110
 Phe Gly Asn Val Gly Pro Gly Leu Thr Ala Ala Leu Asn Asn Ile Gly
 115 120 125
 Phe Gly Asn Thr Gly Ser Asn Asn Ile Gly Phe Gly Asn Thr Gly Ser
 130 135 140
 Asn Asn Ile Gly Phe Gly Asn Thr Gly Asp Gly Asn Arg Gly Ile Gly
 145 150 155 160
 Leu Thr Gly Ser Gly Leu Leu Gly Phe Gly Gly Leu Asn Ser Gly Thr
 165 170 175
 Gly Asn Ile Gly Leu Phe Asn Ser Gly Thr Gly Asn Val Gly Ile Gly
 180 185 190
 Asn Ser Gly Thr Gly Asn Trp Gly Ile Gly Asn Ser Gly Asn Ser Tyr
 195 200 205
 Asn Thr Gly Phe Gly Asn Ser Gly Asp Ala Asn Thr Gly Phe Phe Asn
 210 215 220
 Ser Gly Ile Ala Asn Thr Gly Val Gly Asn Ala Gly Asn Tyr Asn Thr
 225 230 235 240
 Gly Ser Tyr Asn Pro Gly Asn Ser Asn Thr Gly Gly Phe Asn Met Gly

200

245					250					255					
Gln	Tyr	Asn	Thr	Gly	Tyr	Leu	Asn	Ser	Gly	Asn	Tyr	Asn	Thr	Gly	Leu
			260					265					270		
Ala	Asn	Ser	Gly	Asn	Val	Asn	Thr	Gly	Ala	Phe	Ile	Thr	Gly	Asn	Phe
		275					280					285			
Asn	Asn	Gly	Phe	Leu	Trp	Arg	Gly	Asp	His	Gln	Gly	Leu	Ile	Phe	Gly
	290					295					300				
Ser	Pro	Gly	Phe	Phe	Asn	Ser	Thr	Ser	Ala	Pro	Ser	Ser	Gly	Phe	Phe
305						310					315				320
Asn	Ser	Gly	Ala	Gly	Ser	Ala	Ser	Gly	Phe	Leu	Asn	Ser	Gly	Ala	Asn
				325					330					335	
Asn	Ser	Gly	Phe	Phe	Asn	Ser	Ser	Ser	Gly	Ala	Ile	Gly	Asn	Ser	Gly
			340						345				350		
Leu	Ala	Asn	Ala	Gly	Val	Leu	Val	Ser	Gly	Val	Ile	Asn	Ser	Gly	Asn
		355					360					365			
Thr	Val	Ser	Gly	Leu	Phe	Asn	Met	Ser	Leu	Val	Ala	Ile	Thr	Thr	Pro
	370					375					380				
Ala	Leu	Ile	Ser	Gly	Phe	Phe	Asn	Thr	Gly	Ser	Asn	Met	Ser	Gly	Phe
385						390					395				400
Phe	Gly	Gly	Pro	Pro	Val	Phe	Asn	Leu	Gly	Leu	Ala	Asn	Arg	Gly	Val
				405					410					415	
Val	Asn	Ile	Leu	Gly	Asn	Ala	Asn	Ile	Gly	Asn	Tyr	Asn	Ile	Leu	Gly
			420				425						430		
Ser	Gly	Asn	Val	Gly	Asp	Phe	Asn	Ile	Leu	Gly	Ser	Gly	Asn	Leu	Gly
		435					440					445			
Ser	Gln	Asn	Ile	Leu	Gly	Ser	Gly	Asn	Val	Gly	Ser	Phe	Asn	Ile	Gly
	450					455					460				
Ser	Gly	Asn	Ile	Gly	Val	Phe	Asn	Val	Gly	Ser	Gly	Ser	Leu	Gly	Asn
465						470					475				480
Tyr	Asn	Ile	Gly	Ser	Gly	Asn	Leu	Gly	Ile	Tyr	Asn	Ile	Gly	Phe	Gly
				485					490					495	
Asn	Val	Gly	Asp	Tyr	Asn	Val	Gly	Phe	Gly	Asn	Ala	Gly	Asp	Phe	Asn
			500					505					510		
Gln	Gly	Phe	Ala	Asn	Thr	Gly	Asn	Asn	Asn	Ile	Gly	Phe	Ala	Asn	Thr
		515					520					525			
Gly	Asn	Asn	Asn	Ile	Gly	Ile	Gly	Leu	Ser	Gly	Asp	Asn	Gln	Gln	Gly
	530					535					540				
Phe	Asn	Ile	Ala	Ser	Gly	Trp	Asn	Ser	Gly	Thr	Gly	Asn	Ser	Gly	Leu
545						550					555				560
Phe	Asn	Ser	Gly	Thr	Asn	Asn	Val	Gly	Ile	Phe	Asn	Ala	Gly	Thr	Gly
				565					570					575	

201

Asn Val Gly Ile Ala Asn Ser Gly Thr Gly Asn Trp Gly Ile Gly Asn
 580 585 590
 Pro Gly Thr Asp Asn Thr Gly Ile Leu Asn Ala Gly Ser Tyr Asn Thr
 595 600 605
 Gly Ile Leu Asn Ala Gly Asp Phe Asn Thr Gly Phe Tyr Asn Thr Gly
 610 615 620
 Ser Tyr Asn Thr Gly Gly Phe Asn Val Gly Asn Thr Asn Thr Gly Asn
 625 630 635 640
 Phe Asn Val Gly Asp Thr Asn Thr Gly Ser Tyr Asn Pro Gly Asp Thr
 645 650 655
 Asn Thr Gly Phe Phe Asn Pro Gly Asn Val Asn Thr Gly Ala Phe Asp
 660 665 670
 Thr Gly Asp Phe Asn Asn Gly Phe Leu Val Ala Gly Asp Asn Gln Gly
 675 680 685
 Gln Ile Ala Ile Asp Leu Ser Val Thr Thr Pro Phe Ile Pro Ile Asn
 690 695 700
 Glu Gln Met Val Ile Asp Val His Asn Val Met Thr Phe Gly Gly Asn
 705 710 715 720
 Met Ile Thr Val Thr Glu Ala Ser Thr Val Phe Pro Gln Thr Phe Tyr
 725 730 735
 Leu Ser Gly Leu Phe Phe Phe Gly Pro Val Asn Leu Ser Ala Ser Thr
 740 745 750
 Leu Thr Val Pro Thr Ile Thr Leu Thr Ile Gly Gly Pro Thr Val Thr
 755 760 765
 Val Pro Ile Ser Ile Val Gly Ala Leu Glu Ser Arg Thr Ile Thr Phe
 770 775 780
 Leu Lys Ile Asp Pro Ala Pro Gly Ile Gly Asn Ser Thr Thr Asn Pro
 785 790 795 800
 Ser Ser Gly Phe Phe Asn Ser Gly Thr Gly Gly Thr Ser Gly Phe Gln
 805 810 815
 Asn Val Gly Gly Gly Ser Ser Gly Val Trp Asn Ser Gly Leu Ser Ser
 820 825 830
 Ala Ile Gly Asn Ser Gly Phe Gln Asn Leu Gly Ser Leu Gln Ser Gly
 835 840 845
 Trp Ala Asn Leu Gly Asn Ser Val Ser Gly Phe Phe Asn Thr Ser Thr
 850 855 860
 Val Asn Leu Ser Thr Pro Ala Asn Val Ser Gly Leu Asn Asn Ile Gly
 865 870 875 880
 Thr Asn Leu Ser Gly Val Phe Arg Gly Pro Thr Gly Thr Ile Phe Asn
 885 890 895
 Ala Gly Leu Ala Asn Leu Gly Gln Leu Asn Ile Gly Ser Ala Ser Cys
 900 905 910

Arg Ile Arg His Glu Leu Asp Thr Val Ser Thr Ile Ile Ser Ala Phe
915 920 925

Cys Gly Ser Ala Ser Asp Glu Ser Asn Pro Gly Ser Val Ser Glu
930 935 940

(2) INFORMATION FOR SEQ ID NO:205:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:205:

GGATCCATAT GGGCCATCAT CATCATCATC ACGTGATCGA CATCATCGGG ACC

53

(2) INFORMATION FOR SEQ ID NO:206:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 42 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:206:

CCTGAATTCA GGCCTCGGTT GCGCCGGCCT CATCTTGAAC GA

42

(2) INFORMATION FOR SEQ ID NO:207:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:207:

GGATCCTGCA GGCTCGAAAC CACCGAGCGG T

31

(2) INFORMATION FOR SEQ ID NO:208:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:208:
CTCTGAATTC AGCGCTGGAA ATCGTCGCGA T 31
- (2) INFORMATION FOR SEQ ID NO:209:
- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:209:
GGATCCAGCG CTGAGATGAA GACCGATGCC GCT 33
- (2) INFORMATION FOR SEQ ID NO:210:
- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 38 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:210:
GGATATCTGC AGAATTCAGG TTAAAGCCC ATTTGCGA 38
- (2) INFORMATION FOR SEQ ID NO:211:
- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:211:
CCGCATGCGA GCCACGTGCC CACAACGGCC 30
- (2) INFORMATION FOR SEQ ID NO:212:
- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 37 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:212:

CTTCATGGAA TTCTCAGGCC GGTAAGGTCC GCTGCGG

37

(2) INFORMATION FOR SEQ ID NO:213:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7676 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:213:

TGGCGAATGG GACGCGCCCT GTAGCGGCGC ATTAAGCGCG GCGGGTGTGG TGGTTACGCG	60
CAGCGTGACC GCTACACTTG CCAGCGCCCT AGCGCCCGCT CCTTTCGCTT TCTTCCCTTC	120
CTTTCTCGCC ACGTTGCGCG GCTTTCCCCG TCAAGCTCTA AATCGGGGGC TCCCTTTAGG	180
GTTCCGATTT AGTGCTTTAC GGCACCTCGA CCCCCAAAAA CTTGATTAGG GTGATGGTTC	240
ACGTAGTGGG CCATCGCCCT GATAGACGGT TTTTCGCCCT TTGACGTTGG AGTCCACGTT	300
CTTTAATAGT GGACTCTTGT TCCAAACTGG AACAACACTC AACCCCTATCT CGGTCTATTC	360
TTTTGATTTA TAAGGGATTT TGCCGATTTT GGCCTATTGG TTAAAAATG AGCTGATTTA	420
ACAAAAATTT AACGCGAATT TTAACAAAAT ATTAACGTTT ACAATTTTCA GTGGCACTTT	480
TCGGGGAAAT GTGCGCGGAA CCCCTATTTG TTTATTTTTT TAAATACATT CAAATATGTA	540
TCCGCTCATG AATTAATTCT TAGAAAAACT CATCGAGCAT CAAATGAAAC TGCAATTTAT	600
TCATATCAGG ATTATCAATA CCATATTTTT GAAAAAGCCG TTTCTGTAAT GAAGGAGAAA	660
ACTCACCGAG GCAGTTCCAT AGGATGGCAA GATCCTGGTA TCGGTCTGCG ATTCCGACTC	720
GTCCAACATC AATACAACCT ATTAATTTCC CCTCGTCAAA AATAAGGTTA TCAAGTGAGA	780
AATCACCATG AGTGACGACT GAATCCGGTG AGAATGGCAA AAGTTTATGC ATTTCTTTCC	840
AGACTTGTTT AACAGGCCAG CCATTACGCT CGTCATCAAA ATCACTCGCA TCAACCAAAC	900
CGTTATTCAT TCGTGATTGC GCCTGAGCGA GACGAAATAC GCGATCGCTG TTAAAAGGAC	960
AATTACAAAC AGGAATCGAA TGCAACCGGC GCAGGAACAC TGCCAGCGCA TCAACAATAT	1020
TTTCACCTGA ATCAGGATAT TCTTCTAATA CCTGGAATGC TGTTTTCCCG GGGATCGCAG	1080
TGGTGAGTAA CCATGCATCA TCAGGAGTAC GGATAAAATG CTTGATGGTC GGAAGAGGCA	1140

TAAATTC CGT	CAGCCAGTTT	AGTCTGACCA	TCTCATCTGT	AACATCATTG	GCAACGCTAC	1200
CTTTGCCATG	TTTCAGAAAC	AACTCTGGCG	CATCGGGCTT	CCCATAACAAT	CGATAGATTG	1260
TCGCACCTGA	TTGCCCCGACA	TTATCGCGAG	CCCATTTTATA	CCCATATAAAA	TCAGCATCCA	1320
TGTTGGAATT	TAATCGCGGC	CTAGAGCAAG	ACGTTTCCCG	TTGAATATGG	CTCATAACAC	1380
CCCTTGTATT	ACTGTTTATG	TAAGCAGACA	GTTTTATTGT	TCATGACCAA	AATCCCTTAA	1440
CGTGAGTTTT	CGTTCCACTG	AGCGTCAGAC	CCCGTAGAAA	AGATCAAAGG	ATCTTCTTGA	1500
GATCCTTTTT	TTCTGCGCGT	AATCTGCTGC	TTGCAAACAA	AAAAACCACC	GCTACCAGCG	1560
GTGGTTTGTT	TGCCGGATCA	AGAGCTACCA	ACTCTTTTTTC	CGAAGGTAAC	TGGCTTCAGC	1620
AGAGCGCAGA	TACCAAATAC	TGTCCTTCTA	GTGTAGCCGT	AGTTAGGCCA	CCACTTCAAG	1680
AACTCTGTAG	CACCGCCTAC	ATACCTCGCT	CTGCTAATCC	TGTTACCACT	GGCTGCTGCC	1740
AGTGGCGATA	AGTCGTGTCT	TACCGGGTTG	GACTCAAGAC	GATAGTTACC	GGATAAGGCG	1800
CAGCGGTCGG	GCTGAACGGG	GGGTTCGTGC	ACACAGCCCA	GCTTGGAGCG	AACGACCTAC	1860
ACCGAACTGA	GATACCTACA	GCGTGAGCTA	TGAGAAAGCG	CCACGCTTCC	CGAAGGGAGA	1920
AAGGCGGACA	GGTATCCGGT	AAGCGGCAGG	GTCGGAACAG	GAGAGCGCAC	GAGGGAGCTT	1980
CCAGGGGGAA	ACGCCTGGTA	TCTTTATAGT	CCTGTCGGGT	TTCGCCACCT	CTGACTTGAG	2040
CGTCGATTTT	TGTGATGCTC	GTCAGGGGGG	CGGAGCCTAT	GGAAAAACGC	CAGCAACGCG	2100
GCCTTTTTTAC	GGTTCCTGGC	CTTTTGCTGG	CCTTTTGCTC	ACATGTTCTT	TCCTGCGTTA	2160
TCCCCTGATT	CTGTGGATAA	CCGTATTACC	GCCTTTGAGT	GAGCTGATAC	CGCTCGCCGC	2220
AGCCGAACGA	CCGAGCGCAG	CGAGTCAGTG	AGCGAGGAAG	CGGAAGAGCG	CCTGATGCGG	2280
TATTTTCTCC	TTACGCATCT	GTGCGGTATT	TCACACCGCA	TATATGGTGC	ACTCTCAGTA	2340
CAATCTGCTC	TGATGCCGCA	TAGTTAAGCC	AGTATACACT	CCGCTATCGC	TACGTGACTG	2400
GGTCATGGCT	GCGCCCCGAC	ACCCGCCAAC	ACCCGCTGAC	GCGCCCTGAC	GGGCTTGTCT	2460
GCTCCCGGCA	TCCGCTTACA	GACAAGCTGT	GACCGTCTCC	GGGAGCTGCA	TGTGTCAGAG	2520
GTTTTACCG	TCATACCGA	AACGCGCGAG	GCAGCTGCGG	TAAAGCTCAT	CAGCGTGGTC	2580
GTGAAGCGAT	TCACAGATGT	CTGCCTGTTC	ATCCGCGTCC	AGCTCGTTGA	GTTTCTCCAG	2640
AAGCGTTAAT	GTCTGGCTTC	TGATAAAGCG	GGCCATGTTA	AGGGCGGTTT	TTTCTGTTT	2700
GGTCACTGAT	GCCTCCGTGT	AAGGGGGATT	TCTGTTCATG	GGGGTAATGA	TACCGATGAA	2760
ACGAGAGAGG	ATGCTCACGA	TACGGGTAC	TGATGATGAA	CATGCCCCGT	TACTGGAACG	2820
TTGTGAGGGT	AAACAACCTG	CGGTATGGAT	GCGGCGGGAC	CAGAGAAAAA	TCACTCAGGG	2880
TCAATGCCAG	CGCTTCGTTA	ATACAGATGT	AGGTGTTCCA	CAGGGTAGCC	AGCAGCATCC	2940
TGCGATGCAG	ATCCGGAACA	TAATGGTGCA	GGGCGCTGAC	TTCCGCGTTT	CCAGACTTTA	3000

CGAAACACGG	AAACCGAAGA	CCATTCATGT	TGTTGCTCAG	GTCGCAGACG	TTTTGCAGCA	3060
GCAGTCGCTT	CACGTTTCGCT	CGCGTATCGG	TGATTCATTC	TGCTAACCAG	TAAGGCAACC	3120
CCGCCAGCCT	AGCCGGGTCC	TCAACGACAG	GAGCACGATC	ATGCGCACCC	GTGGGGCCGC	3180
CATGCCGGCG	ATAATGGCCT	GCTTCTCGCC	GAAACGTTTG	GTGGCGGGAC	CAGTGACGAA	3240
GGCTTGAGCG	AGGGCGTGCA	AGATTCCGAA	TACCGCAAGC	GACAGGCCGA	TCATCGTCGC	3300
GCTCCAGCGA	AAGCGGTCCT	CGCCGAAAAT	GACCCAGAGC	GCTGCCGGCA	CCTGTCTTAC	3360
GAGTTGCATG	ATAAAGAAGA	CAGTCATAAG	TGCGGCGACG	ATAGTCATGC	CCCGCGCCCA	3420
CCGGAAGGAG	CTGACTGGGT	TGAAGGCTCT	CAAGGGCATC	GGTCGAGATC	CCGGTGCCTA	3480
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CCTGTCGTGC	CAGCTGCATT	AATGAATCGG	CCAACGCGCG	GGGAGAGGCG	GTTTGCGTAT	3600
TGGGCGCCAG	GGTGGTTTTT	CTTTTCACCA	GTGAGACGGG	CAACAGCTGA	TTGCCCTTCA	3660
CCGCCTGGCC	CTGAGAGAGT	TGCAGCAAGC	GGTCCACGCT	GGTTTGCCCC	AGCAGGCGAA	3720
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ATCCCACTAC	CGAGATATCC	GCACCAACGC	GCAGCCCGGA	CTCGGTAATG	GCGCGCATTG	3840
CGCCAGCGC	CATCTGATCG	TTGGCAACCA	GCATCGCAGT	GGGAACGATG	CCCTCATTCA	3900
GCATTTGCAT	GGTTTGTTGA	AAACCGGACA	TGGCACTCCA	GTCGCCTTCC	CGTTCCGCTA	3960
TCGGCTGAAT	TTGATTGCGA	GTGAGATATT	TATGCCAGCC	AGCCAGACGC	AGACGCGCCG	4020
AGACAGAACT	TAATGGGCCC	GCTAACAGCG	CGATTTGCTG	GTGACCCAAT	GCGACCAGAT	4080
GCTCCACGCC	CAGTCGCGTA	CCGTCTTCAT	GGGAGAAAAT	AATACTGTTG	ATGGGTGTCT	4140
GGTCAGAGAC	ATCAAGAAAT	AACGCCGGAA	CATTAGTGCA	GGCAGCTTCC	ACAGCAATGG	4200
CATCCTGGTC	ATCCAGCGGA	TAGTTAATGA	TCAGCCCACT	GACGCGTTGC	GCGAGAAGAT	4260
TGTGCACCGC	CGCTTTACAG	GCTTCGACGC	CGCTTCGTTC	TACCATCGAC	ACCACCACGC	4320
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GGGCCAGACT	GGAGGTGGCA	ACGCCAATCA	GCAACGACTG	TTTGCCCGCC	AGTTGTTGTG	4440
CCACGCGGTT	GGGAATGTAA	TTCAGCTCCG	CCATCGCCGC	TTCCACTTTT	TCCCGCGTTT	4500
TCGCAGAAAC	GTGGCTGGCC	TGGTTCACCA	CGCGGGAAAC	GGTCTGATAA	GAGACACCGG	4560
CATACTCTGC	GACATCGTAT	AACGTTACTG	GTTTCACATT	CACCACCCTG	AATTGACTCT	4620
CTTCCGGGCG	CTATCATGCC	ATACCGCGAA	AGGTTTTGCG	CCATTCGATG	GTGTCCGGGA	4680
TCTCGACGCT	CTCCCTTATG	CGACTCCTGC	ATTAGGAAGC	AGCCCAGTAG	TAGGTTGAGG	4740
CCGTTGAGCA	CCGCCGCCGC	AAGGAATGGT	GCATGCAAGG	AGATGGCGCC	CAACAGTCCC	4800
CCGGCCACGG	GGCCTGCCAC	CATACCCACG	CCGAAACAAG	CGCTCATGAG	CCCGAAGTGG	4860

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AATTAATACG	ACTCACTATA	GGGGAATTGT	GAGCGGATAA	CAATTCCCCT	CTAGAAATAA	5040
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CGACATCATC	GGGACCAGCC	CCACATCCTG	GGAACAGGCG	GCGGCGGAGG	CGGTCCAGCG	5160
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GGACAGCGCC	GGCAAGATCA	CCTACCGCAT	CAAGCTCGAA	GTGTCGTTCA	AGATGAGGCC	5280
GGCGCAACCG	AGGGGCTCGA	AACCACCGAG	CGGTTGCGCT	GAAACGGGCG	CCGGCGCCGG	5340
TACTGTGCGG	ACTACCCCCG	CGTCGTGCGC	GGTGACGTTG	GCGGAGACCG	GTAGCACGCT	5400
GCTCTACCCG	CTGTTCAACC	TGTGGGGTCC	GGCCTTTTAC	GAGAGGTATC	CGAACGTCAC	5460
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CAACATTGGG	GCCTCCGACG	CCTATCTGTC	GGAAGGTGAT	ATGGCCGCGC	ACAAGGGGCT	5580
GATGAACATC	GCGCTAGCCA	TCTCCGCTCA	GCAGGTCAAC	TACAACCTGC	CCGGAGTGAG	5640
CGAGCACCTC	AAGCTGAACG	GAAAAGTCCT	GGCGGCCATG	TACCAGGGCA	CCATCAAAAC	5700
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CATTCAAGCC	GCGGCGGCTG	GCTTCGCATC	GAAAACCCCG	GCGAACCAGG	CGATTTTCGAT	6120
GATCGACGGG	CCCGCCCCGG	ACGGCTACCC	GATCATCAAC	TACGAGTACG	CCATCGTCAA	6180
CAACCGGCAA	AAGGACGCCG	CCACCGCGCA	GACCTTGCGG	GCATTTCTGC	ACTGGGCGAT	6240
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GGTGGTGAAG	TTGTCTGACG	CGTTGATCGC	GACGATTTCC	AGCGCTGAGA	TGAAGACCGA	6360
TGCCGCTACC	CTCGCGCAGG	AGGCAGGTAA	TTTCGAGCGG	ATCTCCGGCG	ACCTGAAAAC	6420
CCAGATCGAC	CAGGTGGAGT	CGACGGCAGG	TTCGTTGCAG	GGCCAGTGGC	GCGGCGCGGC	6480
GGGGACGGCC	GCCCAGGCCG	CGGTGGTGCG	CTTCCAAGAA	GCAGCCAATA	AGCAGAAGCA	6540
GGAACCTCGAC	GAGATCTCGA	CGAATATTCT	TCAGGCCGGC	GTCCAATACT	CGAGGGCCGA	6600
CGAGGAGCAG	CAGCAGGCGC	TGTCCTCGCA	AATGGGCTTT	GTGCCACAAA	CGGCCGCCTC	6660
GCCGCCGTCG	ACCGCTGCAG	CGCCACCCGC	ACCGGCGACA	CCTGTTGCCC	CCCCACCACC	6720

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GCTTTACGCC AGCGCCGAAG CCACCGACTC CAAGGCCGCG GCCCGGTTGG GCTCGGACAT 7080
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GGCACC GGCT CCTGCAGAGC CCGCTCCGGC GCCGGCGCCG GCCGGGGAAG TCGCTCCTAC 7440
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ACACTGGCGG CCGCTCGAGC ACCACCACCA CCACCACTGA GATCCGGCTG CTAACAAAGC 7560
CCGAAAGGAA GCTGAGTTGG CTGCTGCCAC CGCTGAGCAA TAACTAGCAT AACCCTTGG 7620
GGCCTCTAAA CGGGTCTTGA GGGGTTTTTT GCTGAAAGGA GGA ACTATAT CCGGAT 7676

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(2) INFORMATION FOR SEQ ID NO:214:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 802 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:214:

```

Met Gly His His His His His Val Ile Asp Ile Ile Gly Thr Ser
1           5           10           15

Pro Thr Ser Trp Glu Gln Ala Ala Ala Glu Ala Val Gln Arg Ala Arg
20           25           30

Asp Ser Val Asp Asp Ile Arg Val Ala Arg Val Ile Glu Gln Asp Met
35           40           45

Ala Val Asp Ser Ala Gly Lys Ile Thr Tyr Arg Ile Lys Leu Glu Val
50           55           60

Ser Phe Lys Met Arg Pro Ala Gln Pro Arg Gly Ser Lys Pro Pro Ser
65           70           75           80

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Gly	Ser	Pro	Glu	Thr	Gly	Ala	Gly	Ala	Gly	Thr	Val	Ala	Thr	Thr	Pro	85	90	95
Ala	Ser	Ser	Pro	Val	Thr	Leu	Ala	Glu	Thr	Gly	Ser	Thr	Leu	Leu	Tyr	100	105	110
Pro	Leu	Phe	Asn	Leu	Trp	Gly	Pro	Ala	Phe	His	Glu	Arg	Tyr	Pro	Asn	115	120	125
Val	Thr	Ile	Thr	Ala	Gln	Gly	Thr	Gly	Ser	Gly	Ala	Gly	Ile	Ala	Gln	130	135	140
Ala	Ala	Ala	Gly	Thr	Val	Asn	Ile	Gly	Ala	Ser	Asp	Ala	Tyr	Leu	Ser	145	150	155
Glu	Gly	Asp	Met	Ala	Ala	His	Lys	Gly	Leu	Met	Asn	Ile	Ala	Leu	Ala	165	170	175
Ile	Ser	Ala	Gln	Gln	Val	Asn	Tyr	Asn	Leu	Pro	Gly	Val	Ser	Glu	His	180	185	190
Leu	Lys	Leu	Asn	Gly	Lys	Val	Leu	Ala	Ala	Met	Tyr	Gln	Gly	Thr	Ile	195	200	205
Lys	Thr	Trp	Asp	Asp	Pro	Gln	Ile	Ala	Ala	Leu	Asn	Pro	Gly	Val	Asn	210	215	220
Leu	Pro	Gly	Thr	Ala	Val	Val	Pro	Leu	His	Arg	Ser	Asp	Gly	Ser	Gly	225	230	235
Asp	Thr	Phe	Leu	Phe	Thr	Gln	Tyr	Leu	Ser	Lys	Gln	Asp	Pro	Glu	Gly	245	250	255
Trp	Gly	Lys	Ser	Pro	Gly	Phe	Gly	Thr	Thr	Val	Asp	Phe	Pro	Ala	Val	260	265	270
Pro	Gly	Ala	Leu	Gly	Glu	Asn	Gly	Asn	Gly	Gly	Met	Val	Thr	Gly	Cys	275	280	285
Ala	Glu	Thr	Pro	Gly	Cys	Val	Ala	Tyr	Ile	Gly	Ile	Ser	Phe	Leu	Asp	290	295	300
Gln	Ala	Ser	Gln	Arg	Gly	Leu	Gly	Glu	Ala	Gln	Leu	Gly	Asn	Ser	Ser	305	310	315
Gly	Asn	Phe	Leu	Leu	Pro	Asp	Ala	Gln	Ser	Ile	Gln	Ala	Ala	Ala	Ala	325	330	335
Gly	Phe	Ala	Ser	Lys	Thr	Pro	Ala	Asn	Gln	Ala	Ile	Ser	Met	Ile	Asp	340	345	350
Gly	Pro	Ala	Pro	Asp	Gly	Tyr	Pro	Ile	Ile	Asn	Tyr	Glu	Tyr	Ala	Ile	355	360	365
Val	Asn	Asn	Arg	Gln	Lys	Asp	Ala	Ala	Thr	Ala	Gln	Thr	Leu	Gln	Ala	370	375	380
Phe	Leu	His	Trp	Ala	Ile	Thr	Asp	Gly	Asn	Lys	Ala	Ser	Phe	Leu	Asp	385	390	395
Gln	Val	His	Phe	Gln	Pro	Leu	Pro	Pro	Ala	Val	Val	Lys	Leu	Ser	Asp	405	410	415

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Ala Leu Ile Ala Thr Ile Ser Ser Ala Glu Met Lys Thr Asp Ala Ala
 420 425 430
 Thr Leu Ala Gln Glu Ala Gly Asn Phe Glu Arg Ile Ser Gly Asp Leu
 435 440 445
 Lys Thr Gln Ile Asp Gln Val Glu Ser Thr Ala Gly Ser Leu Gln Gly
 450 455 460
 Gln Trp Arg Gly Ala Ala Gly Thr Ala Ala Gln Ala Ala Val Val Arg
 465 470 475 480
 Phe Gln Glu Ala Ala Asn Lys Gln Lys Gln Glu Leu Asp Glu Ile Ser
 485 490 495
 Thr Asn Ile Arg Gln Ala Gly Val Gln Tyr Ser Arg Ala Asp Glu Glu
 500 505 510
 Gln Gln Gln Ala Leu Ser Ser Gln Met Gly Phe Val Pro Thr Thr Ala
 515 520 525
 Ala Ser Pro Pro Ser Thr Ala Ala Ala Pro Pro Ala Pro Ala Thr Pro
 530 535 540
 Val Ala Pro Pro Pro Ala Ala Ala Asn Thr Pro Asn Ala Gln Pro
 545 550 555 560
 Gly Asp Pro Asn Ala Ala Pro Pro Pro Ala Asp Pro Asn Ala Pro Pro
 565 570 575
 Pro Pro Val Ile Ala Pro Asn Ala Pro Gln Pro Val Arg Ile Asp Asn
 580 585 590
 Pro Val Gly Gly Phe Ser Phe Ala Leu Pro Ala Gly Trp Val Glu Ser
 595 600 605
 Asp Ala Ala His Phe Asp Tyr Gly Ser Ala Leu Leu Ser Lys Thr Thr
 610 615 620
 Gly Asp Pro Pro Phe Pro Gly Gln Pro Pro Pro Val Ala Asn Asp Thr
 625 630 635 640
 Arg Ile Val Leu Gly Arg Leu Asp Gln Lys Leu Tyr Ala Ser Ala Glu
 645 650 655
 Ala Thr Asp Ser Lys Ala Ala Ala Arg Leu Gly Ser Asp Met Gly Glu
 660 665 670
 Phe Tyr Met Pro Tyr Pro Gly Thr Arg Ile Asn Gln Glu Thr Val Ser
 675 680 685
 Leu Asp Ala Asn Gly Val Ser Gly Ser Ala Ser Tyr Tyr Glu Val Lys
 690 695 700
 Phe Ser Asp Pro Ser Lys Pro Asn Gly Gln Ile Trp Thr Gly Val Ile
 705 710 715 720
 Gly Ser Pro Ala Ala Asn Ala Pro Asp Ala Gly Pro Pro Gln Arg Trp
 725 730 735
 Phe Val Val Trp Leu Gly Thr Ala Asn Asn Pro Val Asp Lys Gly Ala

740				745				750							
Ala	Lys	Ala	Leu	Ala	Glu	Ser	Ile	Arg	Pro	Leu	Val	Ala	Pro	Pro	Pro
		755					760					765			
Ala	Pro	Ala	Pro	Ala	Pro	Ala	Glu	Pro	Ala	Pro	Ala	Pro	Ala	Pro	Ala
	770					775					780				
Gly	Glu	Val	Ala	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Gln	Arg	Thr	Leu
785					790					795					800
Pro	Ala														

CLAIMS

1. A polypeptide comprising an immunogenic portion of a soluble *M. tuberculosis* antigen, or a variant of said antigen that differs only in conservative substitutions and/or modifications, wherein said antigen has an N-terminal sequence selected from the group consisting of:

- (a) Asp-Pro-Val-Asp-Ala-Val-Ile-Asn-Thr-Thr-Cys-Asn-Tyr-Gly-Gln-Val-Val-Ala-Ala-Leu; (SEQ ID No. 120)
- (b) Ala-Val-Glu-Ser-Gly-Met-Leu-Ala-Leu-Gly-Thr-Pro-Ala-Pro-Ser; (SEQ ID No. 121)
- (c) Ala-Ala-Met-Lys-Pro-Arg-Thr-Gly-Asp-Gly-Pro-Leu-Glu-Ala-Ala-Lys-Glu-Gly-Arg; (SEQ ID No. 122)
- (d) Tyr-Tyr-Trp-Cys-Pro-Gly-Gln-Pro-Phe-Asp-Pro-Ala-Trp-Gly-Pro; (SEQ ID No. 123)
- (e) Asp-Ile-Gly-Ser-Glu-Ser-Thr-Glu-Asp-Gln-Gln-Xaa-Ala-Val; (SEQ ID No. 124)
- (f) Ala-Glu-Glu-Ser-Ile-Ser-Thr-Xaa-Glu-Xaa-Ile-Val-Pro; (SEQ ID No. 125)
- (g) Asp-Pro-Glu-Pro-Ala-Pro-Pro-Val-Pro-Thr-Thr-Ala-Ala-Ser-Pro-Pro-Ser; (SEQ ID No. 126)
- (h) Ala-Pro-Lys-Thr-Tyr-Xaa-Glu-Glu-Leu-Lys-Gly-Thr-Asp-Thr-Gly; (SEQ ID No. 127)
- (i) Asp-Pro-Ala-Ser-Ala-Pro-Asp-Val-Pro-Thr-Ala-Ala-Gln-Leu-Thr-Ser-Leu-Leu-Asn-Ser-Leu-Ala-Asp-Pro-Asn-Val-Ser-Phe-Ala-Asn; (SEQ ID No. 128) and
- (j) Ala-Pro-Glu-Ser-Gly-Ala-Gly-Leu-Gly-Gly-Thr-Val-Gln-Ala-Gly; (SEQ ID No. 136)

wherein Xaa may be any amino acid.

2. A polypeptide comprising an immunogenic portion of an *M. tuberculosis* antigen, or a variant of said antigen that differs only in conservative

substitutions and/or modifications, wherein said antigen has an N-terminal sequence selected from the group consisting of:

- (a) Asp-Pro-Pro-Asp-Pro-His-Gln-Xaa-Asp-Met-Thr-Lys-Gly-Tyr-Tyr-Pro-Gly-Gly-Arg-Arg-Xaa-Phe; (SEQ ID No. 129) and
- (b) Xaa-Tyr-Ile-Ala-Tyr-Xaa-Thr-Thr-Ala-Gly-Ile-Val-Pro-Gly-Lys-Ile-Asn-Val-His-Leu-Val; (SEQ ID No. 137), wherein Xaa may be any amino acid.

3. A polypeptide comprising an immunogenic portion of a soluble *M. tuberculosis* antigen, or a variant of said antigen that differs only in conservative substitutions and/or modifications, wherein said antigen comprises an amino acid sequence encoded by a DNA sequence selected from the group consisting of the sequences recited in SEQ ID Nos.: 1, 2, 4-10, 13-25, 52, 99 and 101, the complements of said sequences, and DNA sequences that hybridize to a sequence recited in SEQ ID Nos.: 1, 2, 4-10, 13-25, 52, 99 and 101 or a complement thereof under moderately stringent conditions.

4. A polypeptide comprising an immunogenic portion of a *M. tuberculosis* antigen, or a variant of said antigen that differs only in conservative substitutions and/or modifications, wherein said antigen comprises an amino acid sequence encoded by a DNA sequence selected from the group consisting of the sequences recited in SEQ ID Nos.: 26-51, 138, 139, 163-183 and 201, the complements of said sequences, and DNA sequences that hybridize to a sequence recited in SEQ ID Nos.: 26-51, 138, 139, 163-183 and 201 or a complement thereof under moderately stringent conditions.

5. A DNA molecule comprising a nucleotide sequence encoding a polypeptide according to any one of claims 1-4.

6. An expression vector comprising a DNA molecule according to claim 5.

7. A host cell transformed with an expression vector according to claim 6.

8. The host cell of claim 7 wherein the host cell is selected from the group consisting of *E. coli*, yeast and mammalian cells.
9. A pharmaceutical composition comprising one or more polypeptides according to any one of claims 1-4 and a physiologically acceptable carrier.
10. A pharmaceutical composition comprising one or more DNA molecules according to claim 5 and a physiologically acceptable carrier.
11. A pharmaceutical composition comprising one or more DNA sequences recited in SEQ ID Nos.: 3, 11, 12, 140 and 141; and a physiologically acceptable carrier.
12. A vaccine comprising one or more polypeptides according to any one of claims 1-4 and a non-specific immune response enhancer.
13. A vaccine comprising:
 - a polypeptide having an N-terminal sequence selected from the group consisting of sequences recited in SEQ ID NO: 134 and 135; and
 - a non-specific immune response enhancer.
14. A vaccine comprising:
 - one or more polypeptides encoded by a DNA sequence selected from the group consisting of SEQ ID Nos.: 3, 11, 12, 140 and 141, the complements of said sequences, and DNA sequences that hybridize to a sequence recited in SEQ ID Nos.: 3, 11, 12, 140 and 141; and
 - a non-specific immune response enhancer.
15. The vaccine of claims 12-14 wherein the non-specific immune response enhancer is an adjuvant.

16. A vaccine comprising one or more DNA molecules according to claim 5 and a non-specific immune response enhancer.

17. A vaccine comprising one or more DNA sequences recited in SEQ ID Nos.: 3, 11, 12, 140 and 141; and a non-specific immune response enhancer.

18. The vaccine of claims 16 or 17 wherein the non-specific immune response enhancer is an adjuvant.

19. A pharmaceutical composition according to any one of claims 9-11, for use in the manufacture of a medicament for inducing protective immunity in a patient.

20. A vaccine according to any one of claims 12-18, for use in the manufacture of a medicament for inducing protective immunity in a patient.

21. A fusion protein comprising two or more polypeptides according to any one of claims 1-4.

22. A fusion protein comprising one or more polypeptides according to any one of claims 1-4 and ESAT-6.

23. A fusion protein comprising one or more polypeptides according to any one of claims 1-4 and the *M. tuberculosis* antigen 38 kD (SEQ ID NO:155).

24. A pharmaceutical composition comprising a fusion protein according to any one of claims 21-23 and a physiologically acceptable carrier.

25. A vaccine comprising a fusion protein according to any one of claims 21-23 and a non-specific immune response enhancer.

26. The vaccine of claim 25 wherein the non-specific immune response enhancer is an adjuvant.

27. A pharmaceutical composition according to claim 24, for use in the manufacture of a medicament for inducing protective immunity in a patient.

28. A vaccine according to claims 25 or 26, for use in the manufacture of a medicament for inducing protective immunity in a patient.

29. A method for detecting tuberculosis in a patient, comprising:

(a) contacting dermal cells of a patient with one or more polypeptides according to any one of claims 1-4; and

(b) detecting an immune response on the patient's skin and therefrom detecting tuberculosis in the patient.

30. A method for detecting tuberculosis in a patient, comprising:

(a) contacting dermal cells of a patient with a polypeptide having an N-terminal sequence selected from the group consisting of sequences recited in SEQ ID NO: 134 and 135; and

(b) detecting an immune response on the patient's skin and therefrom detecting tuberculosis in the patient.

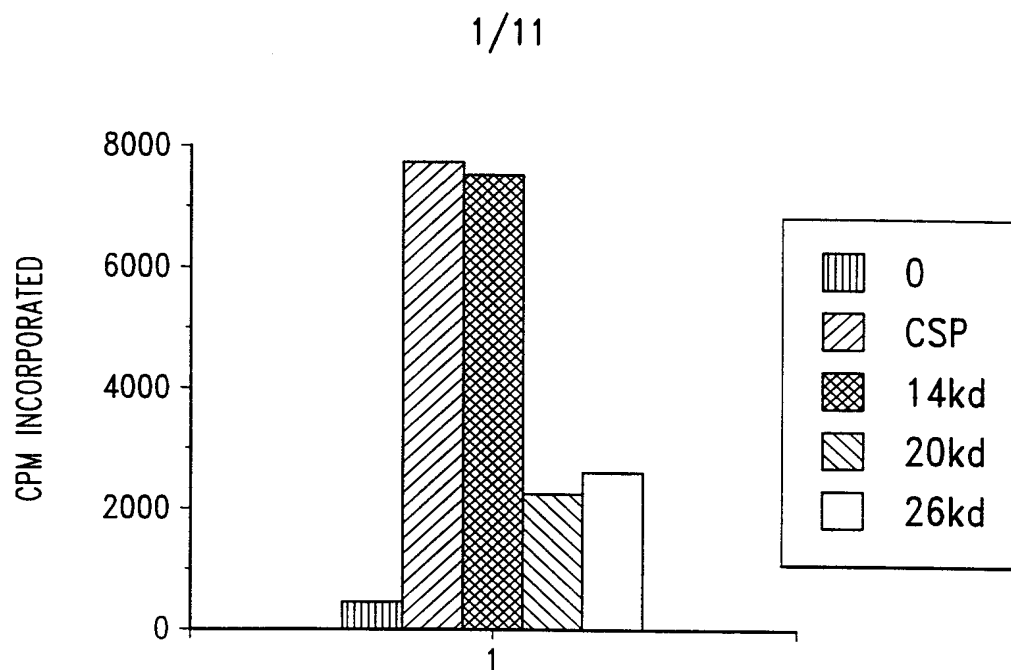
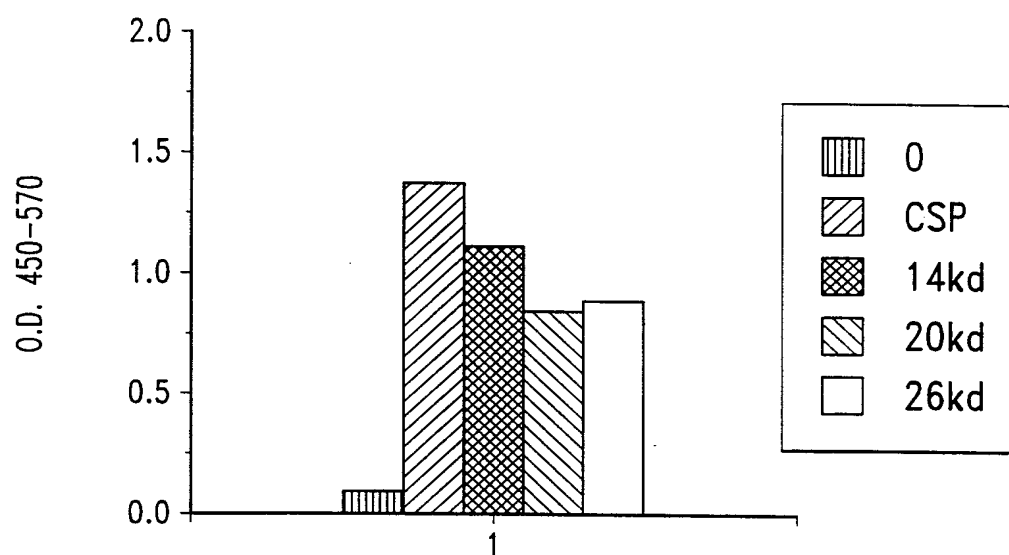
31. A method for detecting tuberculosis in a patient, comprising:

(a) contacting dermal cells of a patient with one or more polypeptides encoded by a DNA sequence selected from the group consisting of SEQ ID Nos.: 3, 11, 12, 140, 141, 156-160, 189-193, 199, 200 and 203, the complements of said sequences, and DNA sequences that hybridize to a sequence recited in SEQ ID Nos.: 3, 11, 12, 140, 141, 156-160, 189-193, 199, 200 and 203; and

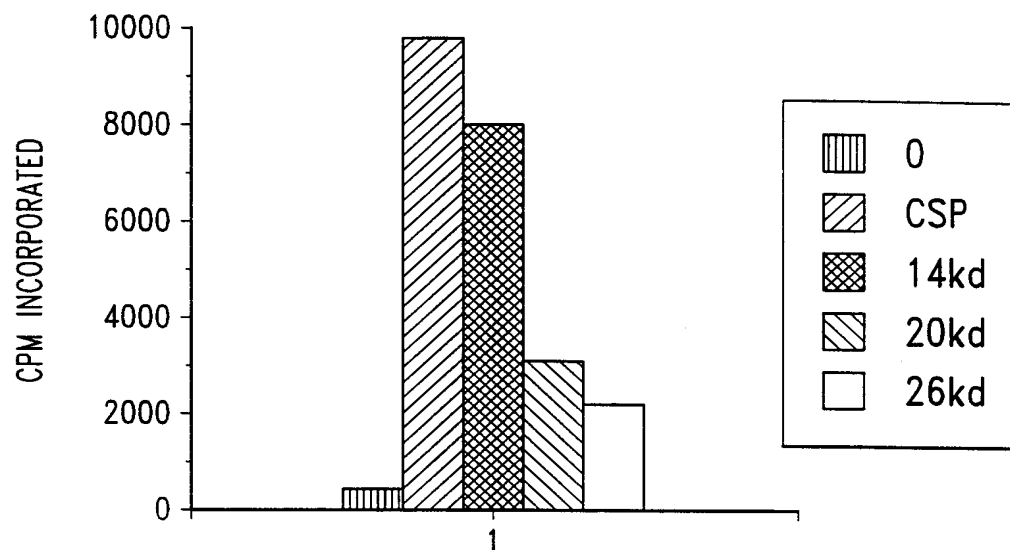
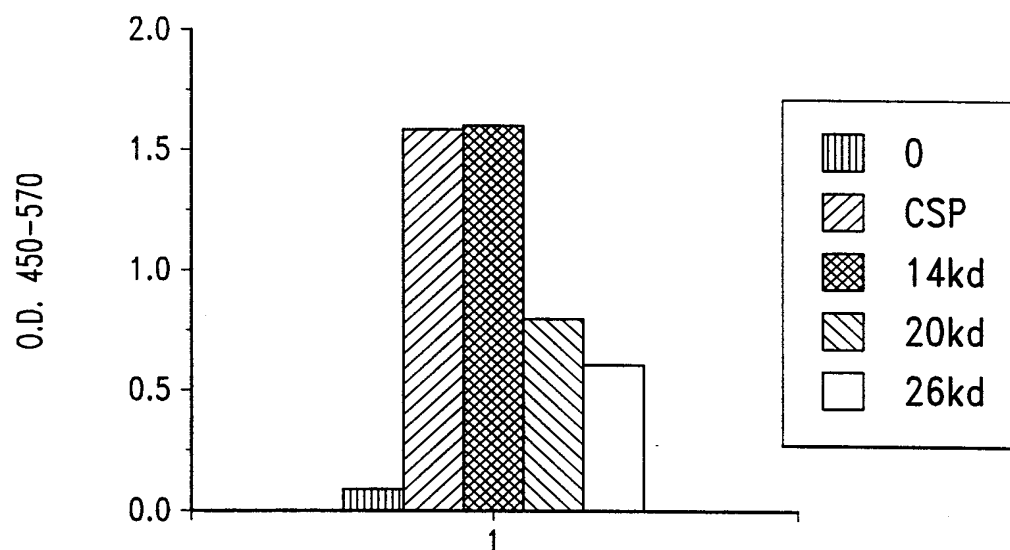
(b) detecting an immune response on the patient's skin and therefrom detecting tuberculosis in the patient.

32. The method of any one of claims 29-31 wherein the immune response is induration.

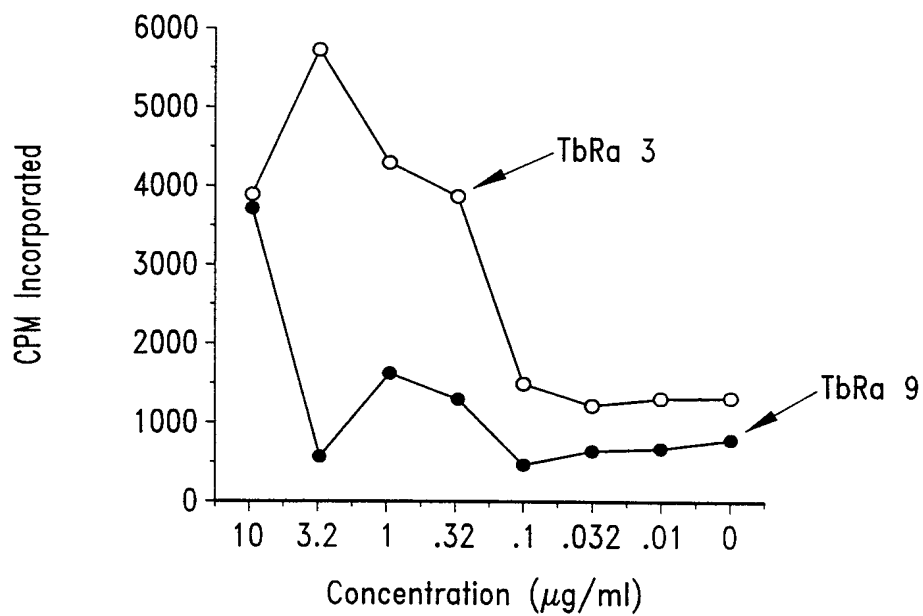
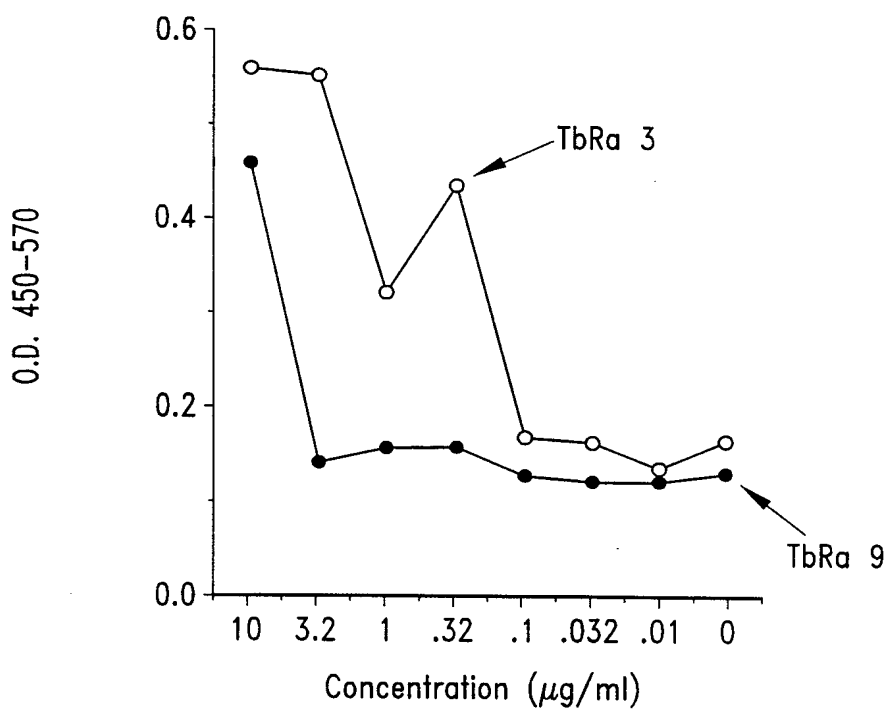
33. A diagnostic kit comprising:
- (a) a polypeptide according to any one of claims 1-4; and
 - (b) apparatus sufficient to contact said polypeptide with the dermal cells of a patient.
34. A diagnostic kit comprising:
- (a) a polypeptide having an N-terminal sequence selected from the group consisting of sequences recited in SEQ ID NO: 134 and 135; and
 - (b) apparatus sufficient to contact said polypeptide with the dermal cells of a patient.
35. A diagnostic kit comprising:
- (a) a polypeptide encoded by a DNA sequence selected from the group consisting of SEQ ID Nos.: 3, 11, 12, 140, 141, 156-160, 189-193, 199, 200 and 203, the complements of said sequences, and DNA sequences that hybridize to a sequence recited in SEQ ID Nos.: 3, 11, 12, 140, 141, 156-160, 189-193, 199, 200 and 203; and
 - (b) apparatus sufficient to contact said polypeptide with the dermal cells of a patient.
36. A diagnostic kit comprising:
- (a) a fusion protein according to any one of claims 21-23; and
 - (b) apparatus sufficient to contact said fusion protein with the dermal cells of a patient.
37. A fusion protein according to claim 23 comprising an amino acid sequence selected from the group consisting of sequences recited in SEQ ID NO: 153 and 209.

*Fig. 1A-1**Fig. 1A-2*

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*Fig. 1B-1**Fig. 1B-2*

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*Fig. 2A**Fig. 2B*

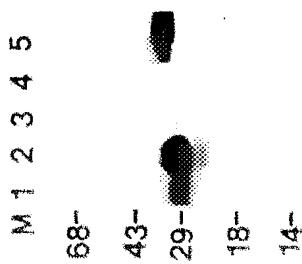


Fig. 3B



Fig. 3D

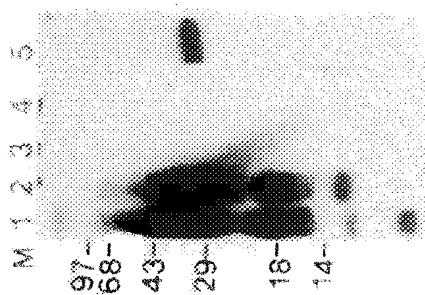


Fig. 3A

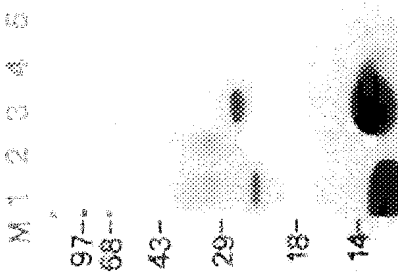


Fig. 3C

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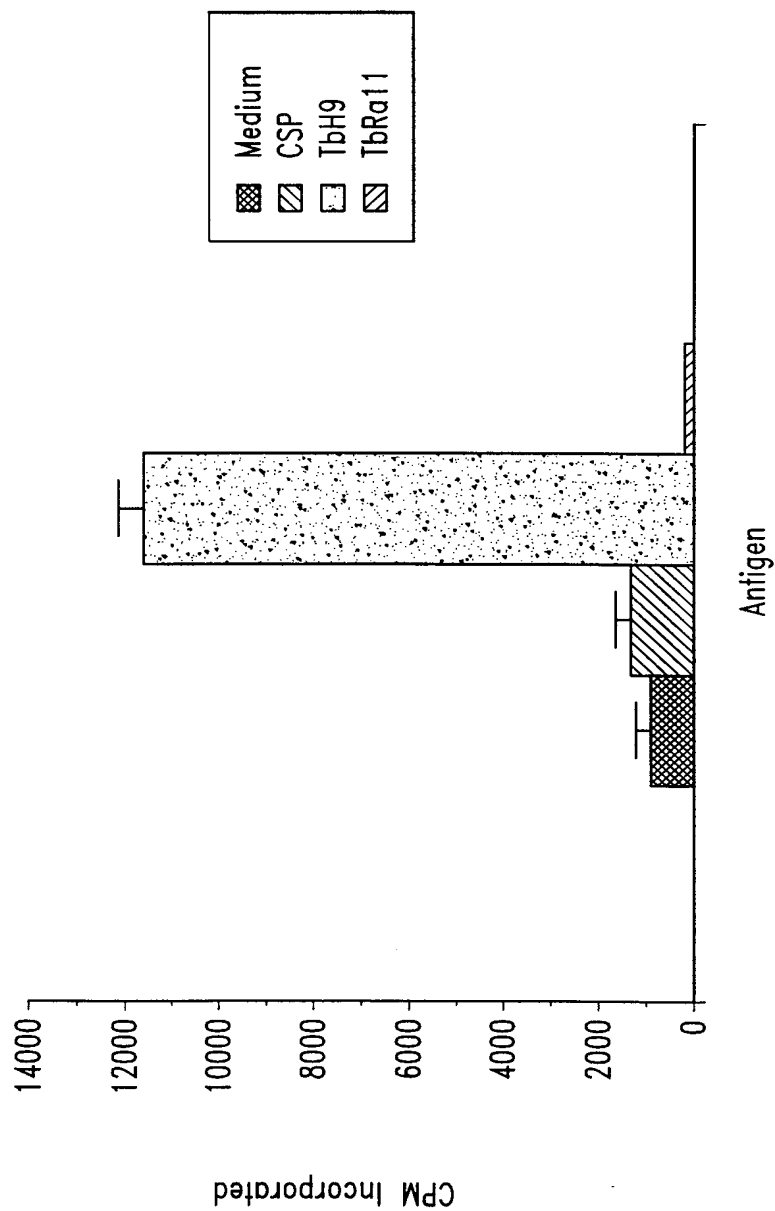
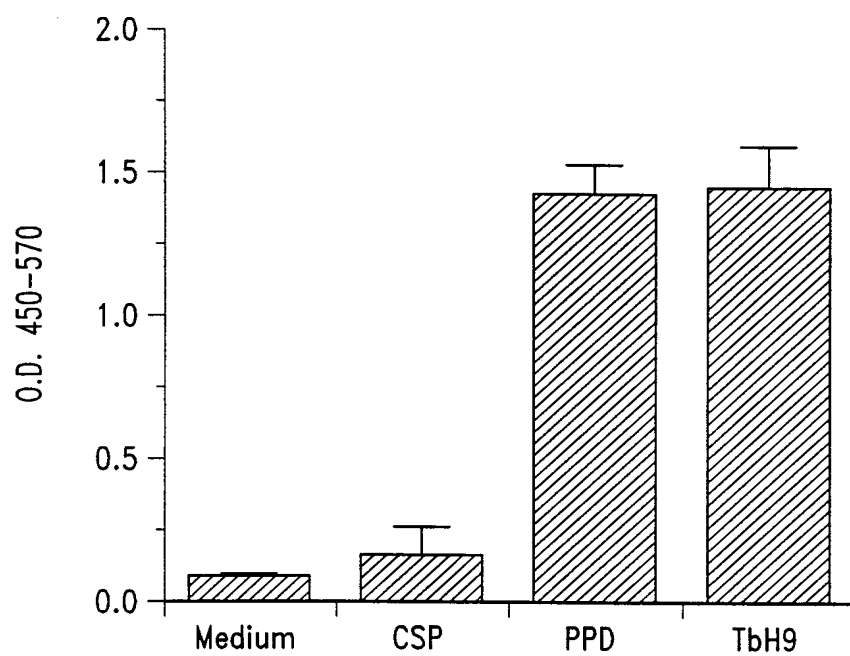
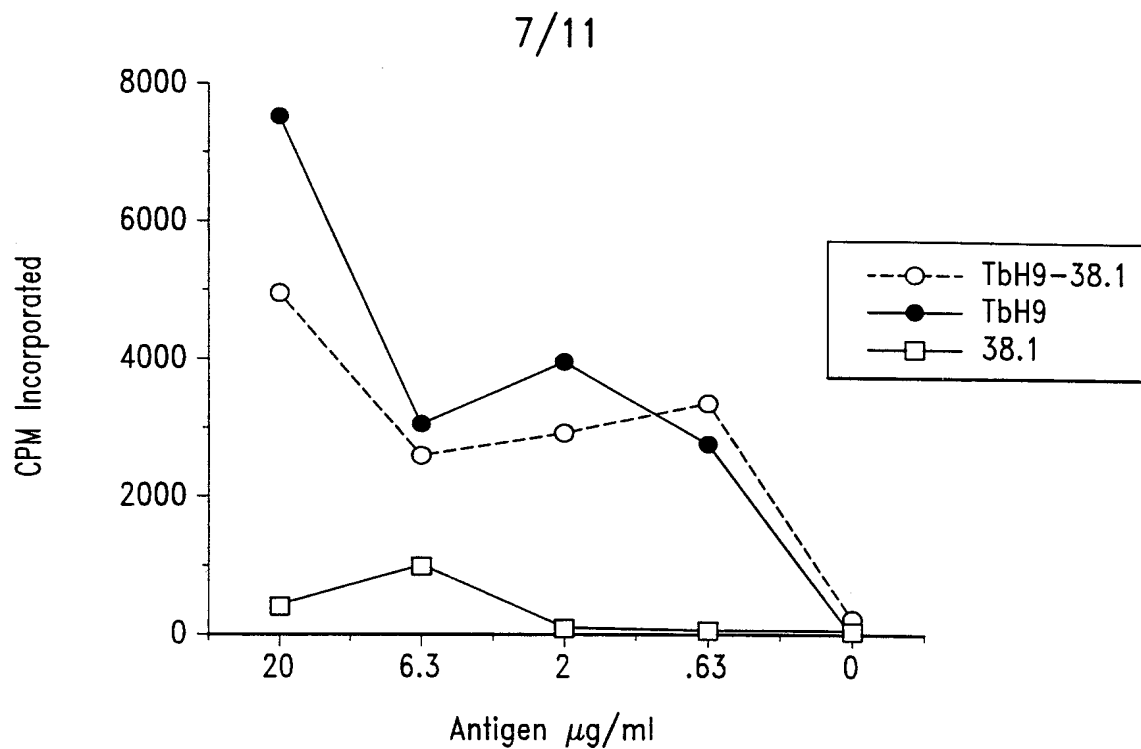
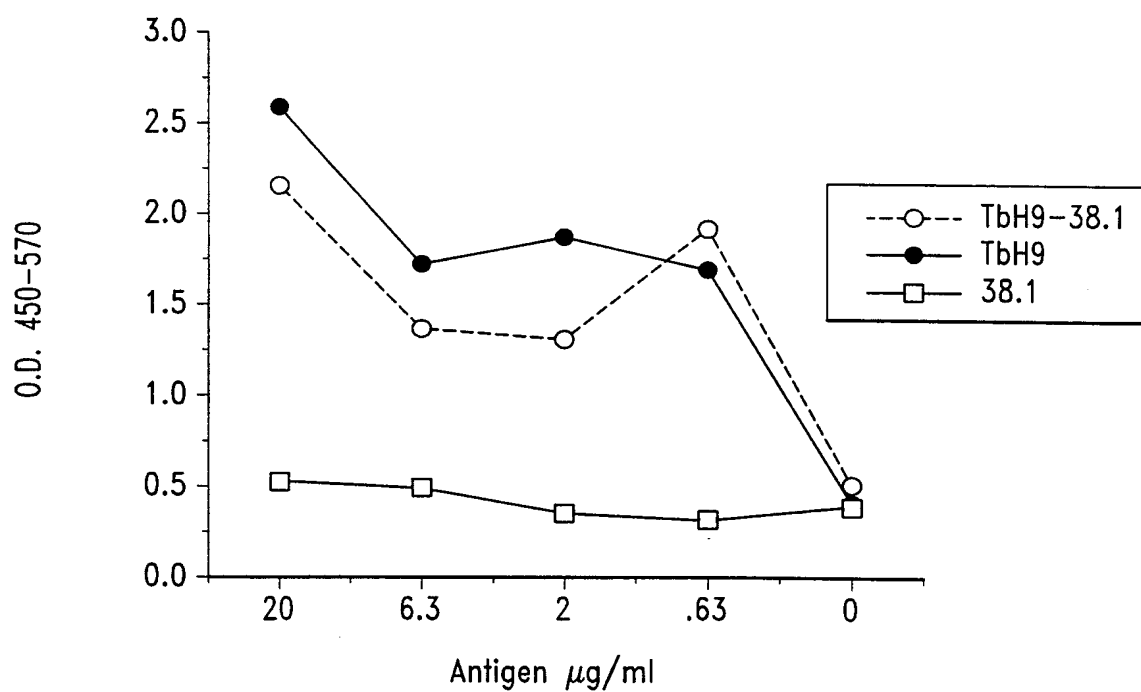
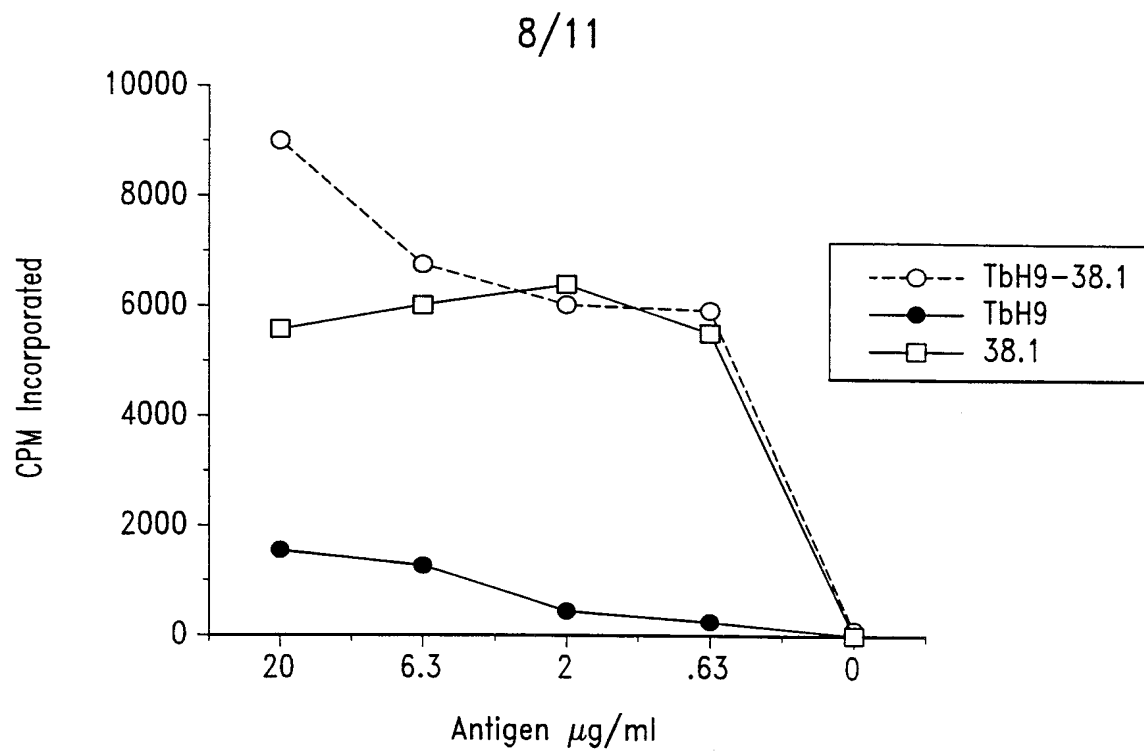
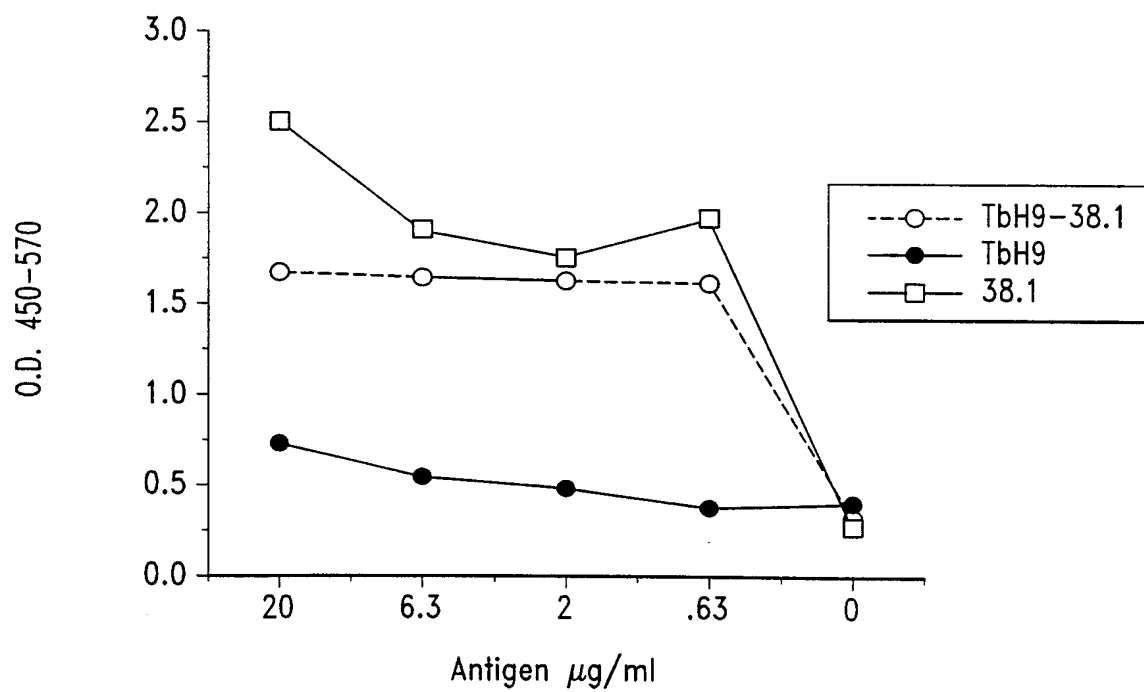


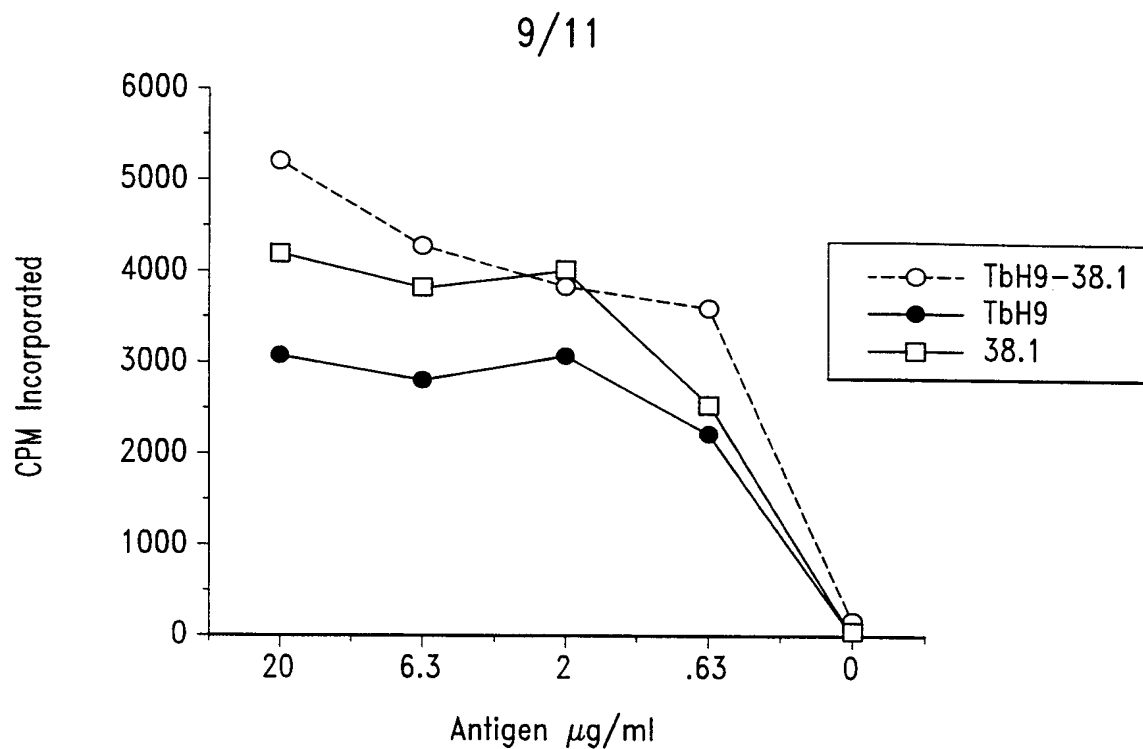
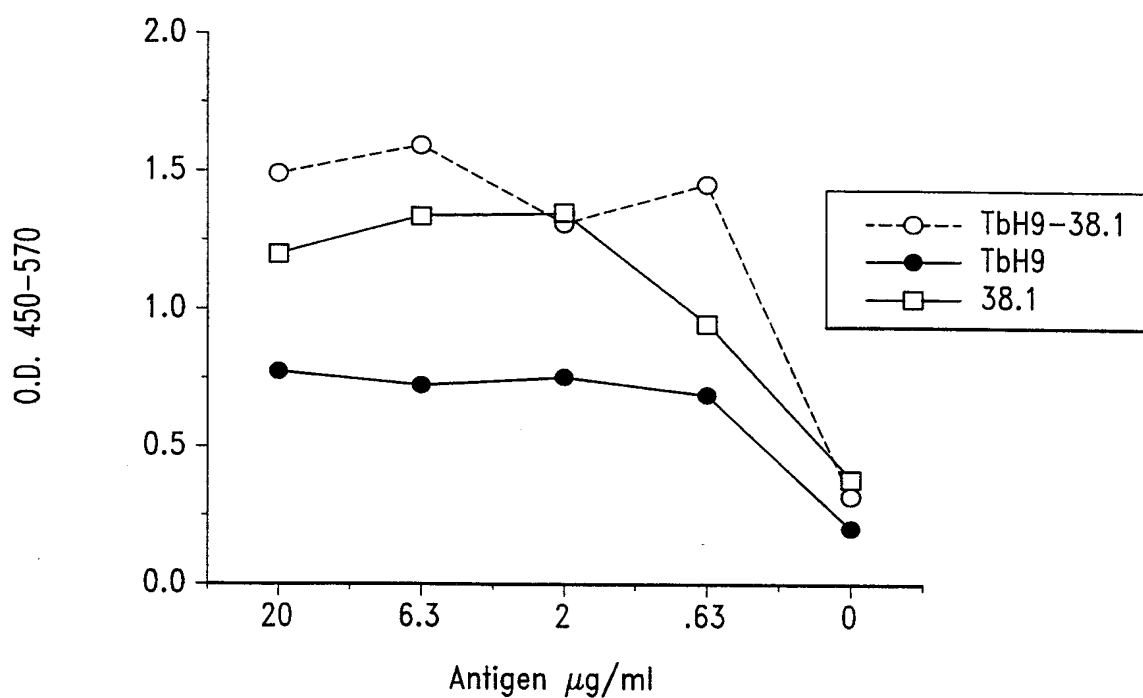
Fig. 4A

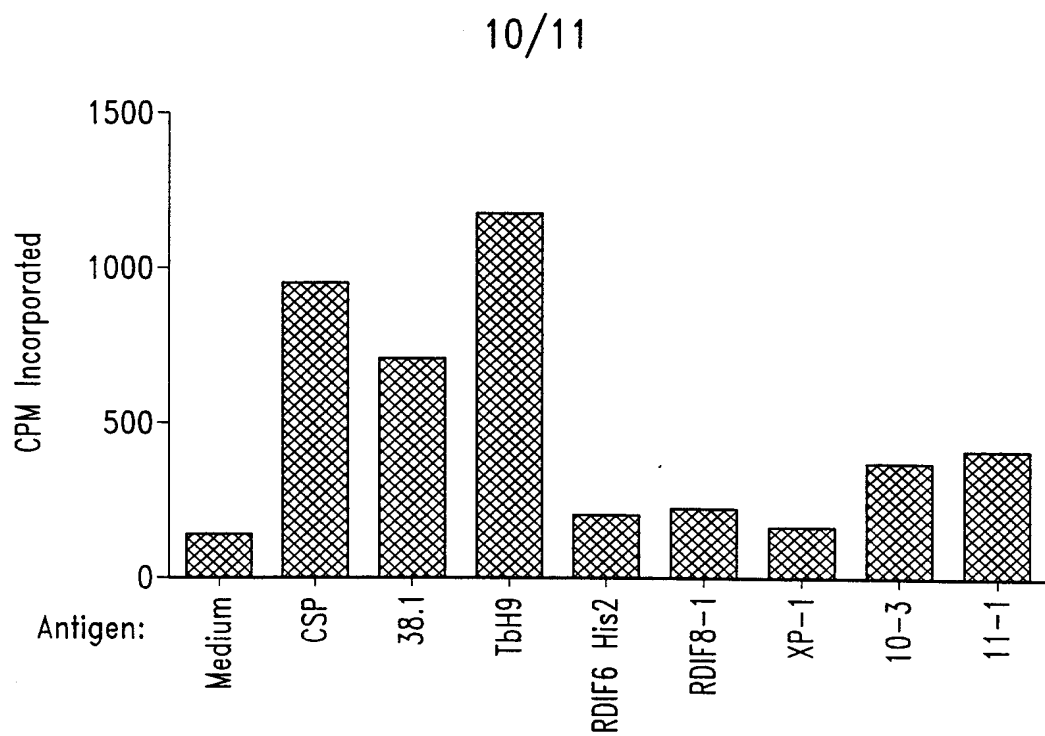
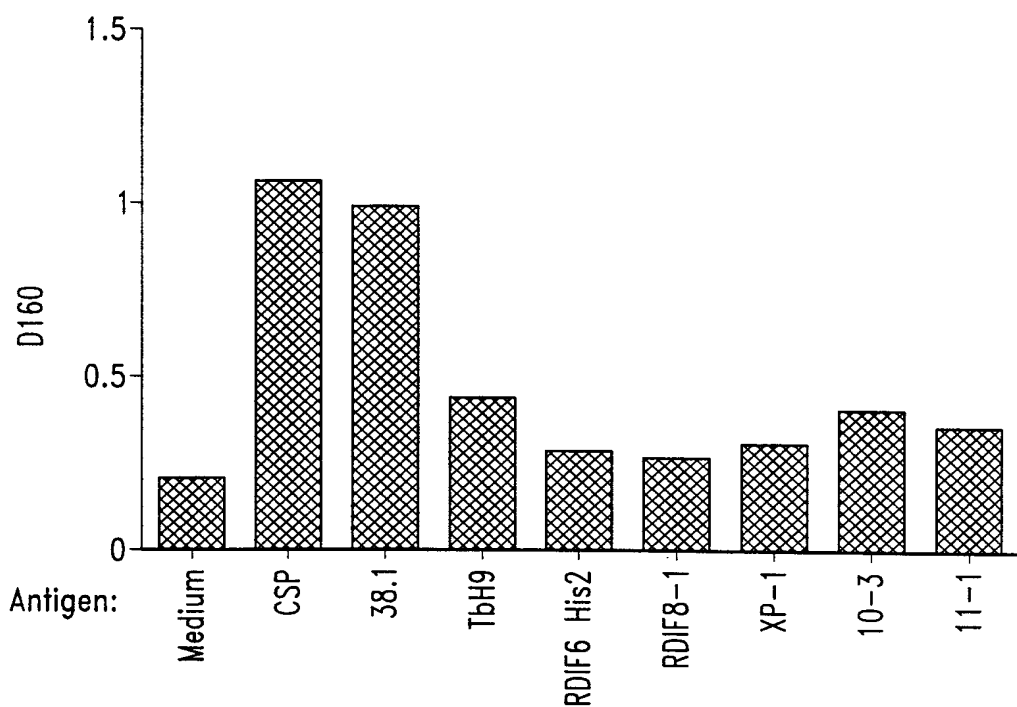
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*Fig. 4B*

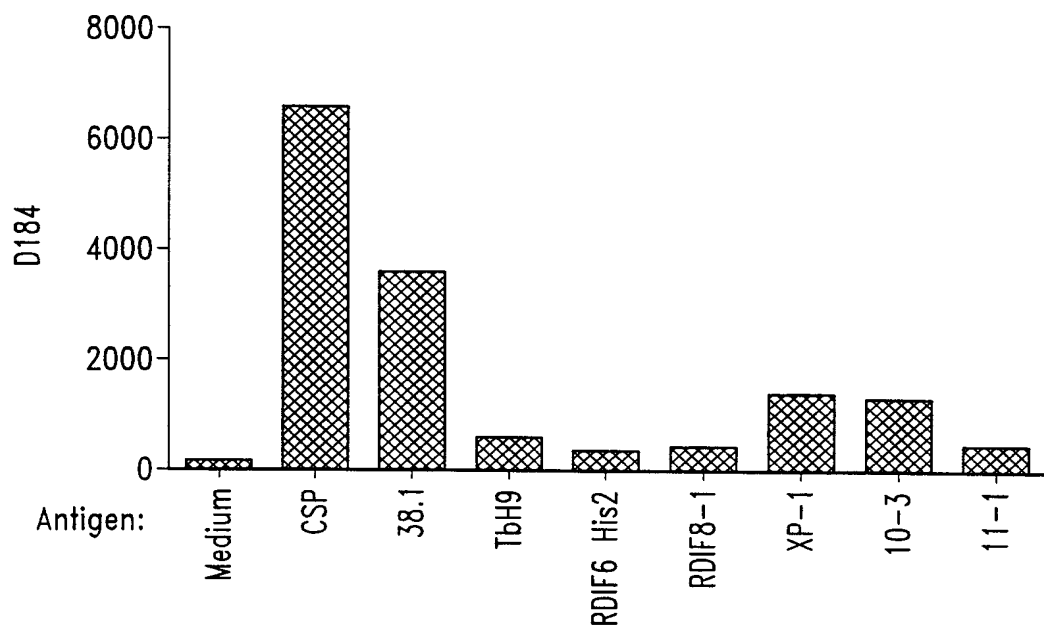
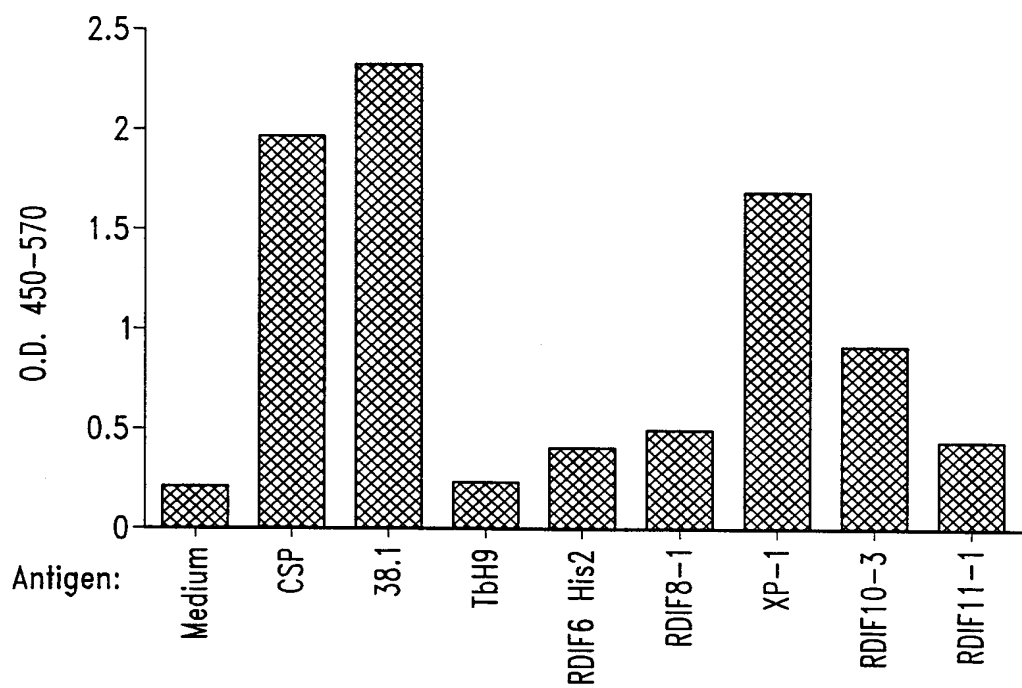
*Fig. 5A**Fig. 5B*

*Fig. 6A**Fig. 6B*

*Fig. 7A**Fig. 7B*

*Fig. 8A**Fig. 8B*

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*Fig. 9A**Fig. 9B*